

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse-Human hybrid fusion protein

<400> 147  
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ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagta catgcactgg 180  
taccagcaga atccaggatc ctcccccaaa cctctggattt atgccccatc caacctggct 240  
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ccacagttcg gtgctgggac caagctggag ctgaaaagtg gcgctggctc gggcgggtgt 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480  
aggcctgggg cctcagtgaa gatgtcctgc aaggtctctg gctacacatt taccagttac 540  
aatagtcact ggtatacttc ctacaatcag cagggtcctg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatctc ccagcacagc ctacatgcag ctacagcagg tgacatctga agactctgag 720  
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ccaaaaccca aggaaccctc catgatctcc cggaacctct aggtcacatg cgtgtgtgtg 960  
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caaatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtgttcagc 1080  
gtctctaccg tcttcgacca ggactggctg aatggcaagg agtacaagtg caaggtcttc 1140  
aaccaaagcc acatcgagaaa catcgagaaa acaatctcca aagccaaagg gcagcctcga 1200  
gaaccacagg tgtacacctc gccccatctc cgggatgagc tgaccaagaa ccaggtcagc 1260  
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<210> 148  
<211> 499  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mouse-Human hybrid fusion protein

<400> 148  
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser

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65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
130 135 140 145  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
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Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220  
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225 230 235 240  
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys  
260 265 270  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
275 280 285  
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
290 295 300  
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305 310 315 320  
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
325 330 335  
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
340 345 350  
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
355 360 365  
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
370 375 380  
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
385 390 395 400  
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
405 410 415  
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
420 425 430 435  
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
440 445 450  
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
455 460 465  
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
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485 490 495  
Pro Gly Lys

<210> 149

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

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aatatgcact gggtaaaaga gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaactcag aagtcaagg gcaaggccac actgactgta 660
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<210> 150

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 150

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20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190     195
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
200     205     210
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
215     220     225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
230     235     240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys

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 Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu  
 305 310 315 320  
 Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly  
 325 330 335  
 Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser  
 340 345 350  
 Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met  
 355 360 365  
 Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys  
 370 375 380  
 Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn  
 385 390 395 400  
 Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys  
 405 410 415  
 Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His  
 420 425 430  
 Ser Ser Ala Lys Pro Cys Gly Gln Ser Ile His Leu Gly Gly Val  
 435 440 445  
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro  
 450 455 460  
 Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys  
 465 470 475 480  
 Leu Glu

<210> 151  
 <211> 1290  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mouse-Human hybrid fusion protein

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 ccaggggaga aggtcacat aattgtcagg gccagctcaa gtgtaagtta catgactgg 180  
 taccagagata agccaggatt ctcgccaaa ccttggaatt atgcccatt caactgggt 240  
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 agcagagtgg aggtgaaga tgcgtccact tattactgcc agcagtgag tttaaccca 360  
 cccacgtctg gtgctgggac caagctggag ctgaagggtg gcggtggctt gggcgggtgt 420  
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 aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actcagtgtg 660  
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<210> 152  
 <211> 422  
 <212> PRT  
 <213> Artificial Sequence

<220>

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<223> Mouse-Human hybrid fusion protein

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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Leu Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Thr Lys
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
260 265 270
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
275 280 285
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
290 295 300
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
305 310 315 320
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
325 330 335
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
340 345 350
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
355 360 365
Ala Asn Thr His Ser Ser Ala Pro Cys Gly Gln Gln Ser Ile His
370 375 380
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
385 390 395 400
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
405 410 415
Gly Leu Leu Lys
420

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<210> 153  
<211> 3630  
<212> DNA  
<213> Homo sapiens

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<400> 153
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cgcgcgctg agaaccgccc ggaacgcacg tgggcgcgcg gcgttcccc cgttccacg 180
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http://www.uspto.gov/ncs/mst

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<210> 154

<211> 595

<212> PRT

<213> Homo sapiens

<400> 154

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 Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys

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65 70 75

Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr  
85 90 95

Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met  
100 105 110

Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His  
115 120 125

Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Gly Thr Ala Gln  
130 135 140

Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys  
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 Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln Val Tyr Leu  
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<213> Homo sapiens

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 10 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp  
 15 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu  
 20 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 25 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser  
 30 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu  
 35 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro  
 40 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu  
 45 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro  
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Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
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<212> DNA
<213> Homo sapiens

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35      40      45
Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50      55      60
Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65      70      75      80
His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85      90      95
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100     105     110
Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115     120     125
Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
130     135     140
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145     150     155     160
Pro Val Thr Arg Gly Ala Gly Ala Gly Arg Gln Arg Gly Gln Asn
165     170     175
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Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr  
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Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val  
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 Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val  
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 Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
 180 185 190  
 Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
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 Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg  
 210 215 220  
 Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn  
 225 230 235 240  
 Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile  
 245 250 255  
 Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
 260 265 270  
 Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly  
 275 280 285  
 Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala  
 290 295 300  
 Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala  
 305 310 315 320  
 Leu Lys Thr Ile Gln Asn Gln Leu Arg Gly Lys Ile Phe Ala Ile Glu  
 325 330 335  
 Gly Thr Gln Thr Gly Ser Ser Ser Phe Glu His Glu Met Ser Gln  
 340 345 350  
 Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
 355 360 365  
 Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
 370 375 380  
 Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
 385 390 395 400  
 Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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 435 440 445  
 Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
 450 455 460  
 Asp Val Asp Ser Asn Gly Thr Asp Leu Val Ile Gly Ala Pro  
 465 470 480  
 His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro  
 485 490 495  
 Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Gly  
 500 505 510  
 Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
 515 520 525  
 Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
 530 535 540  
 Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
 545 550 555  
 Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser  
 560 565 570  
 Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
 580 585 590  
 Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly  
 595 600 605  
 His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
 610 615 620  
 Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
 625 630 635 640  
 Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
 645 650 655  
 His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
 660 665 670  
 Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
 675 680 685  
 Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
 690 695 700  
 Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
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 Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
 725 730 735  
 Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
 740 745 750  
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 770 775 780  
 Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
 785 790 795 800  
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 820 825 830  
 Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
 835 840 845  
 Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
 850 855 860  
 Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
 865 870 875 880  
 Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
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 900 905 910  
 Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
 915 920 925  
 Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
 930 935 940  
 Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn  
 945 950 955 960  
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<400> 178  
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35 40 45

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val  
85 90 95  
Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val  
100 105 110  
Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Lys Ile  
115 120 125  
Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu  
130 135 140  
Ser Ser Leu Arg Leu Asn Val Ser Trp Ala Thr Gly Arg Ser Trp  
145 150 155  
Leu Ala Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser  
160 165 170 175  
Ile Ala Gln Ala His Ser Pro Ala Phe Ser Cys Glu Gln Val Arg Ala  
180 185 190  
Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly  
195 200 205  
Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile  
210 215 220  
Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val  
225 230 235 240  
Cys Ala Ala Leu Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu  
245 250 255  
Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys  
260 265 270  
Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu  
275 280 285  
Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu  
290 295 300  
Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu  
305 310 315 320  
Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr  
325 330 335  
Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys  
340 345 350  
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Gln Gly Ala Arg Gly Phe Ala  
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<210> 179

<211> 2633

<212> DNA

<213> Homo sapiens

<400> 179

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caccgacgcc ggcattttaca agtgtgtggt tacaggcgag gatggcagtg agtcagaggc 360  
cgactcaac gtgaagatct ttcagaagct catgttcaag aatgcgcaaa cccacagga 420  
gttcgggag gggaagaatg ccgtgattgt gtgtgatgtg gtcagctccc tcccaccaac 480  
catcatcttg aaacacaaag gccgagatgt catctgaaa aaagatgtcc gattcatagt 540  
cctgtcccaac aactaccctgc agatccgggg catcaagaaa acagatgagg gcattattcg 600  
ctgtgagggc agaattcctgg caggggggga gatcaacttc aggacattc aggtcattgt 660  
gatgtgtcca cctaccatcc gggccaggca gaattattgt aatgccaccy ccaactcgg 720  
ccagtcctgc accctgtgtg gcgatgccga acggttccca gagcccaaca tgagctggac 780  
aaaggtggg gaacagatag agcaagagga agcagatgag aagtacatct tcagcgagca 840  
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caattacagc	aatatcaaga	tctacaacac	ccctctgcc	agctatctgg	aggtgacccc	1440
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gtctctcgaa	ttcatcccttg	ttcaagcaga	caccctctct	tcaccatcca	ctgaccaggt	1560
ggagccatca	ttcagca cag	cccaggtgca	gtttgatgaa	ccagaggcca	caggtggggt	1620
ggccatcttc	aaataca aag	ctgagtgga	agcagtggtg	gaagaagtat	ggcattccaa	1680
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cccaaacatg	gatggaggga	aacacacaga	gcccaacgag	accacgccac	tgacggagcc	2460
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<210> 180  
<211> 848  
<212> PRT  
<213> Homo sapiens

<400> 180  
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20 25 30  
Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys  
35 40 45  
Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro  
50 55 60  
Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Ser Ser Ser Thr  
65 70 75  
Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys  
80 85 90 95  
Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val  
100 105 110  
Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu  
115 120 125  
Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser  
130 135 140  
Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu  
145 150 155  
Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile  
160 165 170 175  
Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg  
180 185 190  
Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val  
195 200 205  
Asn Val Pro Pro Thr Ile Arg Ala Arg Gln Asn Ile Val Asn Ala Thr  
210 215 220  
Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Arg Phe  
225 230 235 240  
Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln  
245 250 255  
Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu  
260 265 270  
Thr Ile Lys Lys Val Asp Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile  
275 280 285  
Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Thr Ile His Leu Lys Val

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Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu  
340 345 350  
Lys Thr Leu Asp Gly His Met Val Arg Ser His Ala Arg Val Ser  
355 360 365  
Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile  
370 375 380  
Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu  
385 390 395 400  
Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr  
405 410 415  
Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro  
420 425 430 435  
Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser  
440 445 450  
Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu  
455 460 465  
Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr  
470 475 480  
Ala Val Asn Arg Ile Gly Gln Glu Ser Phe Glu Phe Ile Leu Val Gln  
485 490 495  
Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Tyr Ser  
500 505 510  
Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val  
515 520 525  
Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val  
530 535 540  
Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile  
545 550 555  
Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu  
560 565 570  
Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu  
575 580 585 590  
Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu  
595 600 605  
Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys  
610 615 620  
Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg  
625 630 635 640  
Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser  
645 650 655 660  
Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Gly Val  
665 670 675  
Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe  
680 685 690  
Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser  
695 700 705  
Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val  
710 715 720  
Ile Phe Val Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu  
725 730 735  
Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys  
740 745 750  
Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala  
755 760 765  
Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu  
770 775 780  
Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn  
785 790 795 800  
Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys  
805 810 815  
Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Glu Val Lys  
820 825 830  
Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala  
835 840 845

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<210> 181
<211> 1702
<212> DNA
<213> Homo sapiens

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gaaggggtct tccaagttcc tctcattgct ccatcaccatt caataccaca 300
ttaatcatag ctctcattgc ctatcagctg gccaataaca aggtctgggt tggctaccag 360
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aggaatgtct actttatttc tactgtgaag aggtctgggt cttcagccca aatgtcttgt 420
ctgcaacatg gtgtcactct tgctgtcatt gattctgaaa aggtctgggt ctttctaaaa 480
cgatagcgag gttagagaga acactgggtt gactctgaaa aggtctgggt taccatcggt 540
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actcaaggaa atctgtgtca gtggatgctg ctctgtggct cgaagtcttc catagagact 780
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aaggagaata ttccaggaaa gtgccaaaga ttgagaagaat gactatgcaa cctttggatgt 960
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aaaaaaaaaa aaaaaaaa aa 1702

<210> 182
<211> 199
<212> PRT
<213> Homo sapiens

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35 40 45
Val Phe Ile Thr Ile Leu Ile Ile Ala Leu Ile Ala Leu Ser Val Gly
50 55 60
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser
65 70 75 80
His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys
85 90 95
Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala
100 105 110
Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp
115 120 125
Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly
130 135 140
Leu Lys Lys Glu Pro Gly His Pro Trp Lys Trp Ser Asn Gly Lys Glu
145 150 155 160
Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu
165 170 175
Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp
180 185 190
Ile Cys Asn Lys Pro Tyr Lys

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<210> 183  
<211> 1642  
<212> DNA  
<213> Homo sapiens

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tgtgcagcat ttaacgctcat atgtgataat gtggggaagg attggagaag ctgggtcgtg 480
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1500
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<210> 184  
<211> 208  
<212> PRT  
<213> Homo sapiens

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<400> 184
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
1 5 10 15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
80 85 90
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
95 100 105
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
110 115 120
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
125 130 135
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
140 145 150
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
155 160 165
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
170 175 180
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
185 190 195
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
195 200 205

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<210> 185
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 185
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gggtgagatgg cagctctgggca aaatgggcac gaagagtggg tgggcagcgc atacctgttt 120
gtggagctctt cgctggacaa ggtggtcctg tcggatgcct acgcgcaccc ccagcagaag 180
gtggcagatgt acaggtctct gcaggctggc tcggcagaga cgcgcagcgc ccggcagctg 240
ctgcagatgt tgaagtcca ccgcagcgcg ccgcagctga tcgtgcagct gcggtctctg 300
gggcggcagc cctgtggccg ctctctcgcg gcttaccgcg agggggcgct gcgcgccgcg 360
ctgcagaggg gccctggcgg cgcgcctgcc cagcactgcg tgccgctgca actggagctg 420
cgcgcgcggc ccgagcgctt ggagcctttg ctggcggcag aggagcgcgt tttgagttgc 480
atcctagccc agcagcccca ccggtctcgg gatgaagaac tggctgagct ggaagatgcg 540
ctgcgaaatc tgaagtgcgg ctcgggggcc cggggtggcg acggggaggt cgcttcggcc 600
cccttgacgc ccccggtgcc ctctctgtcg gagggtgaag cgcgcgcgcc gccgccacct 660
gccacagact ttctgttcca gggtcagcct gtagtgaatc ggccgcgtag cctcaggagc 720
caacagacgt tcgcgcgctc tgtgggtctc aaatggcgca agtgtggggcg ctactgcag 780
cgaggctgcc gggcgctcgc ggacccggcg ctggactcgc tggcctacga gtacgagcgc 840
gaggggactgt agagcagggc cttccagctg ctgcggcgct tcgtgcaggc cgaggggcgc 900
cgcgccagcg tgcagcgctt ggtggaggca ctgcaggaga acgagctcac cagcctggca 960
gaggacttgc tgggactctg cgtatccaat ggcggcctgg cctagaccag ggggtcagcc 1020
agcttttggg gaactctgat ggcctttaggg ttccttctgc ggctattgct gaacctgttc 1080
catccacggg gaccctgaaa ctccacttgg gctatctgct ggacactgtct gggcagctgt 1140
gattgctctc ccaggagacc agacacttgg ggggtcatca ttggggattc tgccctcaggt 1200
actttgatag agttgtgggt gggggggagc tgctttggag atcagctcca cctgtctcca 1260
tcccagaagc ggggcttaca gccagccctt acagtttcc tcatgaagca cctgtatctt 1320
tgggtctcct gacttcatcc tgggtgctcg agatatcga gtgaagtaaa acaggatca 1380
atcttgcctg ccccagctc acactcagcg tgggaccccg aatgttaagc aatgataata 1440
aagataaca cggaataaaa aaaaaaaaaa aaaaaa 1475

```

```

<210> 186
<211> 312
<212> PRT
<213> Homo sapiens

<400> 186
Met Ala Ala Gly Gln Asn Gly His Glu Glu Trp Val Gly Ser Ala Tyr
1 5 10 15
Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
20 25 30
Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
35 40 45
Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
50 55 60
His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
65 70 75 80
Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
85 90 95
Ala Ala Leu Gln Arg Ser Leu Ala Ala Ala Leu Ala Gln His Ser Val
100 105 110
Pro Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu
115 120 125
Leu Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
130 135 140
Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
145 150 155
Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
160 165 170 175
Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Glu Val Lys Pro
180 185 190
Pro Pro Val Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
195 200 205
Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
210 215 220

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly  
225 230 235 240  
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu Tyr  
245 250 255  
Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe  
260 265 270  
Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala  
275 280 285  
Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu  
290 295 300  
Thr Asp Pro Asn Gly Gly Leu Ala  
305 310

<210> 187  
<211> 600  
<212> DNA  
<213> Homo sapiens

<400> 187  
atggaagcca gagacaagca ggtactccgc tccctgcgtc tggagctggg tgcggaggtg 60  
ctggtggaag gactggctct tcagtagctt taccaggaag gaattttgac agaaaaccac 120  
attcaagaaa tcaaaactca aaccacaggc ctccgggaaga caatgctgtt gctggacatc 180  
ctgccttcca ggggcccaca agcttttgac accttctcg attccctcca ggaatttccc 240  
tgggtaagag agaagctgga gaaggcgaga gaggaagtcg cagccgagct gcctacaggt 300  
gactgtagtg ccggaatccc ctacacatc ctacagcagt cgccatcaga ccagcagatt 360  
aaccagctgg atcagaagct aggcccgagg tgggagcccg tggctcgtgc tctggagctg 420  
tccagacagg acatctaccg ctgcaaggcc aaccatcccc acaacgtgca ttcgaggtg 480  
gtggaggcct ttgtccgctg gcgccagcgt ttggggaagc aggccacctt cctaagctta 540  
cacaagggcc tccaggcagt ggaggctgat ccctccctgc tccagcacat gctggagtga 600

<210> 188  
<211> 199  
<212> PRT  
<213> Homo sapiens

<400> 188  
Met Glu Ala Arg Asp Lys Gln Val Leu Arg Ser Leu Arg Leu Glu Leu  
1 5 10 15  
Gly Ala Glu Val Leu Val Glu Gly Leu Val Leu Gln Tyr Leu Tyr Gln  
20 25 30  
Glu Gly Ile Leu Thr Glu Asn His Ile Gln Glu Ile Lys Ala Gln Thr  
35 40 45  
Thr Gly Leu Arg Lys Thr Met Leu Leu Leu Asp Ile Leu Pro Ser Arg  
50 55 60  
Gly Pro Lys Ala Phe Asp Thr Phe Leu Asp Ser Leu Gln Glu Phe Pro  
65 70 75 80  
Trp Val Arg Glu Lys Leu Glu Lys Ala Arg Glu Glu Val Thr Ala Glu  
85 90 95  
Leu Pro Thr Gly Asp Trp Met Ala Gly Ile Pro Ser His Ile Leu Ser  
100 105 110  
Ser Ser Pro Ser Asp Gln Gln Ile Asn Gln Leu Ala Gln Lys Leu Gly  
115 120 125  
Pro Glu Trp Glu Pro Val Val Leu Ser Leu Gly Leu Ser Gln Thr Asp  
130 135 140  
Ile Tyr Arg Cys Lys Ala Asn His Pro His Asn Val His Ser Gln Val  
145 150 155  
Val Glu Ala Phe Val Arg Trp Arg Gln Arg Phe Gly Lys Gln Ala Thr  
160 165 170  
Phe Leu Ser Leu His Lys Gly Leu Gln Ala Val Glu Ala Asp Pro Ser  
175 180 185 190  
Leu Leu Gln His Met Leu Glu  
195

<210> 189  
<211> 1642  
<212> DNA

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49076.000004ptc2 10.207.655 Seq List Text 07.24.03.txt  
<213> Homo sapiens

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<400> 189
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gccagcgagc cgaggacaga gggcgcacgg agggccgggc cgcagccccc gcgccttgca 120
gaccccgcca tggaccctgt cctgggtgctg ctgcactcgg tgtcgtccag cctgtcgagc 180
agcagctcga cggagctcaa gtctctatgc ctgcggcgcg tgggcaagcg caagctggag 240
cgcgtgcaga agctctctcg cgagctgctg atgctgtgctg agcagaacga cctggagccc 300
gggacacacg agctcgaggg gggggcgctg gccctccctgc ggcgccacga cctgctgcgg 360
cgcgtcgarg acttcgaggg gggggcgctg ggcctggggc cgcctgggga agaagacctg 420
tgtgcagcat ttaacgtcat atgtgataat gtggggaagc attggagaag attggagagc 480
cagctcaaaag ttacgagcac caagatcgac agcatcgagg acagataccc ccgcgaacct 540
acagagcggt tgcgggagtc actgagaatc tgcagaatga acctgggtgc tgacctggtg 600
gtggccacc tgggtggggc tctcaggctc tgcagatga gggccatgtc ccgatgtca 720
caagaggttc agcaggcccg tgacctccag aacaggagtg gggccatgtc ccgatgtca 780
tggaactcag agcatactac ctccgaagcg tcctgatggg ccgctgcttt gcgctgtgtg 840
accacagcca tctcacacgc ctggactttg gttctctcca ggaaggtagc ccagcactgt 900
gaagaccagc caggaagcca ggcctgagtg gccacagacc acctgctttc gaactcaagg 960
tgctgtttat aatgcctctc ccgcaccagg ccgggcttgg gccctgcaca gatatttcca 1020
tttcttcttc actatgcacac tgagcaaatg ctgtctcca cagaaggaat ctgtgcagat gacagatcac 1080
tgagtggaaa agtgggaacc cagagcgagc gagaccagct ctgtctcca cagaaggaat ctgtgcagat gacagatcac 1140
actgttactc ctggagcttg aacccccgcc atccttcacc agagcccatg ctcaaacact 1200
aggttgaaga ctgggacttg cagttggcac actaggtgca aagagatggt ttgtcccatc tcttggagg 1260
gtggcgcttc cgtgcccctg cagttggcac aagagatggt ttgtcccatc tcttggagg 1320
ccaccgggac agaccctggc cctgaggaga cctgagtgac ggcggtggc ctctggccag cgaattgaga 1380
ctcgggtggg gctgggagat cctgagtgac ggcggtggc ctctggccag cgaattgaga 1440
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taatatctgt gaggctgcaa tctacagttt ttactctgtt ttatcaaaa tcaactgttt 1560
aggattatgg gtctctgcaa tctacagttt ttactctgtt ttatcaaaa tcaactgttt 1620
tctgataaca gaattgcca ggcagcgagg tctctgtatc ttaaaaagca gtcctcttat 1642
tcctaaagga atcctattaa aa
```

<210> 190

<211> 208

<212> PRT

<213> Homo sapiens

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<400> 190
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
1 5 15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
85 90 95
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
100 105 110
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
115 120 125
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
130 135 140
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
165 170 175
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
180 185 190
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
195 200 205
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<210> 191

<211> 3492

<212> DNA

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49076.000004pct2 1.0.207.655 Seq List Text 07.24.03.txt  
<213> Homo sapiens

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<400> 191
gggagcacat gcccgcctcag agaatactat gaccagacag ctcagatgtg ctcgagcaaa 60
tgctgcgcgg gccaacatgc tgtaccaaga gctcggaac cgtgtgtgtac 120
tctctgtagg acagacacata caccagcttc tggaaactggg ttcccgagtg cttgagctgt 180
ggctccgcgt gctactctga ccagggtgaa gactcgagg gactcgagg acagaaaccg 240
atctgcagct gcaggcccggt cgtgtactgc ggctgtgagc agcaggagggt gtgcccgtgt 300
tgccgcgcgc tgcgcaagtg tctgtcaagcc gatctgtaac gctgtgtgga cagcagcagg aactgaacaa 360
gatatttgcg ggcctccaca gtccc ccaacc cctgtgtgga ccaacacgac ttcatccagc 420
gatgcagctc gacgtccac atccc aacac cctgtgtgga tccctgggaa tgaacagct 480
ccccagccag tctccacag cctctcgtct cctgtgtgga ccccgagggt agtacaacta 540
ccaagcactc tctctcgtct tctcagttgg catga cccag agccttgtt cctgcagaga 780
gactctgcct tctcagttgg actga ttgtg ggtgtgacag cctcgagagg ccccgagagg 840
ggagtgtgta actgtgtgat cctgt ccatg aagcccgggt gtacacagggt ctcggcagct 900
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tgctctcccc aagccagctc ctccaaggag gaatgtgctt tctgtgaggt gctgtgagct 1260
aaggacgagc aggttccccct caccgaagag aagccccctgc gtgagcaagg ttggctgagc 1320
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tgaggctctt tctgtggccaa cagcgagttg ggggcaatgt cttgagccct ttggttttt 1620
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actttgggag aacccccatc agaagcctga ggtctgggaa gctggcgaca ctggggcgag 2040
aacttggtaa accccatct ccaagcctgc gcactccagc ctgaggggaa ctcgttgaa 2100
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gaggttgtag ggagccgaga agaaaaaaa cagaggggccc taactagaaa ttttaaaaa 2220
ctgtctcaaa ctgcatgtcc cagcacttcc acaaaagcaa actctgcag ccccgagct 2280
tggcaagat aacgcacttc cctccgcct tcaactcggg ctttccaggg aatttcagga 2340
ctcaggccaa caagccaacg cctccgcct tcaactcggg ctttccaggg aatttcagga 2400
gctactagcc caccactatc taccctagcc cttcaattc cttggcccca aacgggctgc 2460
cgtagaccct tctctactgc ccaagtgccc agtctgtgtg cctgtctgtg cgtgcgtgt 2520
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tggtacatgt cagcttgatg tggtaagtt cagccttccc tctgtgtgtg cgtgcgtgt 2640
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ggagccagg gtagctgagc gagctgagc gagctgagc gagctgagc gagctgagc 3120
caacagagtg agacctgtc acattggacc gactctgccc gactctgccc gactctgccc 3180
gttcttgcgc agactctgag cactctgagc gactctgagc gactctgagc gactctgagc 3240
cagctctggg agactctgag cactctgagc gactctgagc gactctgagc gactctgagc 3300
tttggagact cgtgtggggc ttgttcccc ttgttcccc ttgttcccc ttgttcccc 3360
aagtttgac ttgtgtctgg acggcatttc ttgttcccc ttgttcccc ttgttcccc 3420
gtcgaaaaaa aa 3492

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<210> 192  
<211> 425  
<212> PRT  
<213> Homo sapiens

<400> 192

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met  
 1 5 10 15  
 Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr  
 20 25 30  
 Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr  
 35 40 45  
 Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys  
 50 55 60  
 Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg  
 65 70 75 80  
 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu  
 85 90 95  
 Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly  
 100 105 110  
 Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys  
 115 120 125  
 Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg  
 130 135 140  
 Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met  
 145 150 155 160  
 Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly  
 165 170 175  
 Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln  
 180 185 190  
 Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
 195 200 205  
 Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu  
 210 215 220  
 Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile  
 225 230 235 240  
 Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu  
 245 250 255  
 Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala  
 260 265 270  
 Arg Gly Thr Gln Gly Pro Glu Gln His Leu Leu Ile Thr Ala Pro  
 275 280 285  
 Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg  
 290 295 300  
 Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser  
 305 310 315 320  
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro  
 325 330 335  
 Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys  
 340 345 350  
 Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr  
 355 360 365  
 Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln  
 370 375 380  
 Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr  
 385 390 395 400  
 Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly  
 405 410 415  
 Val Pro Asp Ala Gly Met Lys Pro Ser  
 420 425

<210> 193  
 <211> 1799  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 ccacgcgctc cgcataaatc agcacgcggc cggagaaccc cgcaatctct gcgcccacaa 60  
 aatacaccca cgtatgccga tctactttaa gggctgaaac ccacgggcct gagagactat 120  
 aagagcgttc cctaccgaca tggaaacaac gggacagaac gccccggccg cttcgggggc 180  
 ccggaagaag ccaggccag gaccaggaga ggcgcgggga gccaggctcg ggctccgggt 240  
 cccaagacc cttgtgctg ttgtcgcgcg ggtcctgctg ttggtctcag ctgagctcgc 300  
 tctgatcacc caacaagacc tagctcccca cgagagagcg gccccaacac aaaagaggtc 360  
 cagccctca gagggattgt gtcacacttg acaccatatt tcagaagacg gttagatttg 420

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq Lic Text 07.24.03.txt  
 catctctctgc aaatatgtgac aggactatag cactcactgg aatgacctcc ttttctgctt 480  
 gcgctgcacc aggtgtgatt cagggtgaagt ggagctaagt cctctgacca cgaccagaaa 540  
 cacagtgtgt cagtgcaag aaggcacctt ccgggaagaa gattctctctg agatgtgccg 600  
 gaagtgtccgc acaggggtgtc ccagagggtat ggtcaagggtc ggtgattgta caccctggag 660  
 tgacatcgaa tgtgtccaca aagaatcagg catcatcata ggagtcacag ttgcagccgt 720  
 agtcttgatt cgtgctgtgt gtgtgtgtgt gtctttactg tggagaagaa tccttctcta 780  
 cctgaaaggc attctgctcag atgtctccaa tgagatctgt agtatcttgc agcccaacca 900  
 acgacactgg acgcaagtgg attgtgtgga atgacctgag ccacaggtg tcaacatgtt 960  
 ggtctccctgg ggtcagagc attgtgtgga atgacctgag ccacaggtg tcaacatgtt 960  
 gtccccggg ggtcagagc attgtgtgga atgacctgag ccacaggtg tcaacatgtt 960  
 gaggtctgtg gttccagcaa cctttgactc tccggcagaa gctgaaaggt ctgagaggag 1020  
 tgactttgca gacttggtgc tccgactgag actctgagac agtgccttca 1080  
 catggacaat gagataaagg tggctaagg tggagagag ctcatgagga agtggggcct 1140  
 cacgatgctg ataaagtggg tcaacaaaac tggagagag ctcatgagga agtggggcct 1140  
 ggatgccttg gagacgtctg gagagagact tgccaagcag aagattgttg ctaagtgtg 1380  
 gagctctgga aagttcatgt atttagaagg taatgcagac tctgcttgt ctaagtgtg 1380  
 attctcttca ggaagtgtga ccttccctgg tttacctttt tcttggaaaa agcccaactg 1440  
 gactcagctc agtaggagaa tgccacaatt gtccatagac cgttactgga agaaactctc 1500  
 ccatcaaca caccaccagt gatggaacat cctgtaacct ttactgcat ttggcattat 1560  
 ttttaaaagc tgaattgtgt aataaggaca attggaatct tcttgatca ttctgtttgt 1620  
 gcgtactttg agatttgggt tggggatgta ttgttttcac agcacttttt tatcctaagt 1680  
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 aaaaaaaag ggcggccgct accttagagt cgacctgag aagcttgccc gccatggcc 1799

<210> 194  
 <211> 411  
 <212> PRT  
 <213> Homo sapiens

<400> 194  
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 20 25 30  
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 35 40 45  
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln  
 50 55 60  
 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
 65 70 75  
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
 80 85 90  
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Phe  
 100 105 110  
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro  
 115 120 125  
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Gly Thr Phe  
 130 135 140  
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys  
 145 150 155  
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
 160 165 170  
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala  
 175 180 185  
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp  
 190 195 200  
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly  
 205 210 215  
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp  
 220 225 230  
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro  
 235 240 245  
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn  
 250 255 260  
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala  
 265 270 275  
 Glu Arg Ser Gln Arg Arg Glu Leu Val Pro Ala Asn Glu Gly Asp  
 280 285 290  
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val

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305 310 315 320  
Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp  
325 330 335  
Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr  
340 345 350  
Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala  
355 360 365  
Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu  
370 375 380  
Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met  
385 390 395 400  
Tyr Leu Glu Gly Asn Ala Asp Ser Ala Leu Ser  
405 410

<210> 195  
<211> 683  
<212> DNA  
<213> Homo sapiens

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ctcttcagg gtgtctgttt ctgtcctgtt ggcaatagct ttggggcttc tgactgcagt 180  
tctcttgagt gtgtctgtat accagtggat cctgtgccag ggcctcaact actccacttg 240  
tgcacagctgt cctagctgcc cagaccgctg gatgaaatat ggtaaccatt gttattattt 300  
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aaacttctca aggatttctt ctaaatagctt tgtgcagaca tgcgtgccca tcaacaaaaa 540  
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gctggccact ggctgttggtg aaa 683

<210> 196  
<211> 189  
<212> PRT  
<213> Homo sapiens

<400> 196  
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Gln Ala Gln Asn Asp Tyr Gly Pro Gln Lys Ser Ser Ser Arg  
20 25 30  
Pro Ser Cys Ser Cys Leu Val Ala Ile Ala Leu Gly Leu Leu Thr Ala  
35 40 45  
Val Leu Leu Ser Val Leu Leu Tyr Gln Trp Ile Leu Cys Gln Gly Ser  
50 55 60  
Asn Tyr Ser Thr Cys Ala Ser Cys Pro Ser Cys Pro Asp Arg Trp Met  
65 70 75 80  
Lys Tyr Gly Asn His Cys Tyr Tyr Phe Ser Val Glu Glu Lys Asp Trp  
85 90 95  
Asn Ser Ser Leu Glu Phe Cys Leu Ala Arg Asp Ser His Leu Val  
100 105 110  
Ile Thr Asp Asn Gln Glu Met Ser Leu Leu Gln Val Phe Leu Ser Glu  
115 120 125  
Ala Phe Cys Trp Ile Gly Leu Arg Asn Asn Ser Gly Trp Arg Trp Glu  
130 135 140  
Asp Gly Ser Pro Leu Asn Phe Ser Arg Ile Ser Ser Asn Ser Phe Val  
145 150 155 160  
Gln Thr Cys Gly Ala Ile Asn Lys Asn Gly Leu Gln Ala Ser Ser Cys  
165 170 175  
Glu Val Pro Leu His Trp Val Cys Lys Lys Val Arg Leu  
180 185

<210> 197  
<211> 2967  
<212> DNA

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<213> Homo sapiens

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<400> 197
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agggagtcct cggggacacc ctcggcagca gcggagatgc ctctttttgc caccactccc 240
ttcgatcagg atgtgtgagaa agcaaccagc gagatgaata ctgtctagga ctggggcctc 300
attcttgata tctgtgataa agttggtcag tctcgacgtg ctatgcaggc gacctaaaga ttgctctcgg 360
ctatgataga cgtgtaccaa cgtattaaat aagggtcatc ttcaagaatg tccacgatct tggctctcag 420
tttgatagtg agttaagcaa gacagatgaa ggagttacgt aggatccctg tactgtgctt 480
aaggctctta tggttgaatg taaggaacaa aagccagctc cttgtagcca tgctctctca ggaacaaagg 540
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cagttctcatc ttggaagcaat agaatcacag cccagtgatg atcagccaga ctaccagagg 1260
gattgtgata gaaaacattc agaatcacag cccagtgatg atcagccaga ctaccagagg 1320
ctcttatata ccaagttatc attattatgc gactgtctgt gttctctgtt ctccagtgta tgcagctcac 1380
aatcagccat aattattatc gttctctgtt gttctctgtt ctccagtgta tgcagctcac 1440
ctcccaagtg gtgctctact gttctctgtt gttctctgtt ctccagtgta tgcagctcac 1500
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gcagataact gctaaatgct atctctccag gtcacaagtt ctaaatattc aagaaggtag 1920
tttatcctca gcttatagga aactttttag agtttctctt cccccgcccc ctccagtgat 2040
aactctcttc ttacaacatt taattctctt cataatgta aagaattgat acaaagtgtt 2100
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aatggaaata agtagatgtt tcaaagt

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<210> 198  
<211> 540  
<212> PRT  
<213> Homo sapiens

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<400> 198
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20 25 30
Cys Asp Lys Val Gly Gln Ser Arg Thr Gly Pro Lys Asp Cys Leu Arg
35 40 45
Ser Ile Met Arg Arg Val Asn His Lys Asp Pro His Val Ala Met Gln
50 55 60
Ala Leu Thr Leu Leu Gly Ala Cys Val Ser Asn Cys Gly Lys Ile Phe

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65      70      75
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      85      90      95
Leu Asn Lys Gly His Pro Lys Val Cys Glu Lys Leu Lys Ala Leu Met
      100      105      110
Val Glu Trp Thr Asp Glu Phe Lys Asn Asp Pro Gln Leu Ser Leu Ile
      115      120      125
Ser Ala Met Ile Lys Asn Leu Lys Glu Gln Gly Val Thr Phe Pro Ala
      130      135      140
Ile Gly Ser Gln Ala Ala Glu Gln Ala Lys Ala Ser Pro Ala Leu Val
      145      150      155
Ala Lys Asp Pro Gly Thr Val Ala Asn Lys Lys Glu Glu Asp Leu
      160      165      170
Ala Lys Ala Ile Glu Leu Ser Leu Lys Glu Gln Arg Gln Gln Ser Thr
      175      180      185
Thr Leu Ser Thr Leu Tyr Pro Ser Thr Ser Ser Leu Leu Thr Asn His
      190      195      200
Gln His Glu Gly Arg Lys Val Arg Ala Ile Tyr Asp Phe Glu Ala Ala
      205      210      215
Glu Asp Asn Glu Leu Thr Phe Lys Ala Gly Glu Ile Ile Thr Val Leu
      220      225      230
Asp Asp Ser Asp Pro Asn Trp Trp Lys Gly Glu Thr His Gln Gly Ile
      235      240      245
Gly Leu Phe Pro Ser Asn Phe Val Thr Ala Asp Leu Thr Ala Glu Pro
      250      255      260
Glu Met Ile Lys Thr Glu Lys Lys Thr Val Gln Phe Ser Asp Asp Val
      265      270      275
Gln Val Glu Thr Ile Glu Pro Glu Pro Glu Pro Ala Phe Ile Asp Glu
      280      285      290
Asp Lys Met Asp Gln Leu Leu Gln Met Leu Gln Ser Thr Asp Pro Ser
      295      300      305
Asp Asp Gln Pro Asp Leu Pro Glu Leu Leu His Leu Glu Ala Met Cys
      310      315      320
His Gln Met Gly Pro Leu Ile Asp Glu Lys Leu Glu Asp Ile Asp Arg
      325      330      335
Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys Val Met Glu Ala Leu
      340      345      350
Ser Leu Tyr Thr Lys Leu Met Asn Glu Asp Pro Met Tyr Ser Met Tyr
      355      360      365
Ala Lys Leu Gln Asn Gln Pro Tyr Tyr Met Ser Ser Gly Val Ser
      370      375      380
Gly Ser Gln Val Tyr Ala Gly Pro Pro Pro Ser Gly Ala Tyr Leu Val
      385      390      395
Ala Gly Asn Ala Gln Met Ser His Leu Gln Ser Tyr Ser Leu Pro Pro
      400      405      410
Glu Gln Leu Ser Ser Leu Ser Gln Ala Val Val Pro Pro Ser Ala Asn
      415      420      425
Pro Ala Leu Pro Ser Gln Gln Thr Gln Ala Ala Tyr Pro Asn Thr Met
      430      435      440
Val Ser Ser Val Gln Gly Asn Thr Tyr Pro Ser Gln Ala Pro Val Tyr
      445      450      455
Ser Pro Pro Pro Ala Ala Thr Ala Ala Ala Thr Ala Asp Val Thr
      460      465      470
Leu Tyr Gln Asn Ala Gly Pro Asn Met Pro Gln Val Pro Asn Tyr Asn
      475      480      485
Leu Thr Ser Ser Thr Leu Pro Gln Pro Gly Gly Ser Gln Gln Pro Pro
      490      495      500
Gln Pro Gln Gln Pro Tyr Ser Gln Lys Ala Leu Leu
      505      510      515
530      535      540

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<210> 199  
 <211> 2531  
 <212> DNA  
 <213> Homo sapiens

<400> 199  
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 tggtaaaaat cttagttcat gtgaagaaat ttcargtga ttttttagt atcaaacagc 180  
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 aaaaacttaa gagtataatg gaagatagca cgaattgtgc agattggaca aacagcaaca 300  
 aacaaaataa gaagtatgac ttttcctgtg aactctacag aatgtctaca tattcaactt 360  
 tccccgcgg ggtgctctgc tcagaaaagg gtcctgtcgt tgcgtgtttt tattatactt 420  
 gtgtgaatga caaggtcaaa tgcttctgtt gtggcctgat gctggataac tggaaacatg 480  
 gagacagtc ttttcaaaag cataaacagc tatatcttag ctgtagcttt attcagaatc 540  
 tggtttcagc tagtctggga tccacctcta agaatacgtc tccaatgaga aacagttttg 600  
 cacattcatt atctcccacc ttggaacata gtgactgttt cagtgtttct tactcagcc 660  
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 ataagaactt atttggatg agaaatctga acagataatc agaaattgac gtttcaggct 1860  
 gtgtcttcca tctctgtgtg atcttcaaaa agtatattcc aactgtttaa gtgtgtatg 1920  
 atgaactctt atttggatg agaaatctga agtatattcc aactgtttaa gtgtgtatg 1980  
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 atgaactctt atttggatg agaaatctga agtatattcc aactgtttaa gtgtgtatg 2160  
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<210> 200  
 <211> 618  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr  
 35 40 45  
 Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu  
 50 55 60  
 Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys  
 65 70 75 80  
 Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly  
 85 90 95  
 Asp Ser Pro Ile Gln Lys His Lys Gln Tyr Thr Ser Cys Ser Phe  
 100 105 110  
 Ile Gln Asn Leu Val Ser Ala Ser Leu Gly Ser Thr Ser Lys Asn Thr  
 115 120 125  
 Ser Pro Met Arg Asn Ser Phe Ala His Ser Leu Ser Pro Thr Leu Glu  
 130 135 140  
 His Ser Ser Leu Phe Ser Gly Ser Tyr Ser Ser Leu Ser Pro Asn Pro  
 145 150 155 160  
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165 170 175  
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180 185  
Met Trp Pro Leu Thr Phe Leu Ser Pro Ser Glu Leu Ala Arg Ala Gly  
195 200 205  
Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys Gly  
210 215 220  
Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asp Ala Met Ser Glu His  
225 230 235 240  
Arg Arg His Phe Pro Asn Cys Pro Phe Leu Glu Asn Ser Leu Gly Thr  
245 250 255  
Leu Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr His Ala Arg  
260 265 270  
Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro Val Gln Pro Glu  
275 280 285  
Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp Asp Val  
290 295 300  
Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser Gly Asp  
305 310 315 320  
Asp Pro Trp Val Glu His Ala Lys Trp Phe Asp Arg Cys Glu Phe Leu  
325 330 335  
Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile Gln Gly Arg Tyr  
340 345 350  
Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Thr Thr Gly Glu  
355 360 365  
Glu Asn Ala Asp Pro Pro Ile His Phe Gly Pro Gln Ser Ser  
370 375 380  
Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu  
385 390 395 400  
Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Gln Ser Lys  
405 410 415  
Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser  
420 425 430  
Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Glu Lys Glu Lys  
435 440 445  
Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn  
450 455 460  
Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp  
465 470 475 480  
Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile  
485 490 495  
Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr  
500 505 510  
Ile Leu Val Lys Gly Asn Ala Ala Asn Ile Phe Lys Asn Cys Leu  
515 520 525  
Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn  
530 535 540  
Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu  
545 550 555 560  
Gln Leu Arg Arg Leu Gln Glu Arg Thr Cys Lys Val Cys Met Asp  
565 570 575  
Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val Cys  
580 585 590  
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Ile Lys Gly Thr Val Arg Thr Phe Leu Ser  
610 615

<210> 201  
<211> 2477  
<212> DNA  
<213> Homo sapiens

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caaatgacat acatggaagc gaatcaatgg actctggaat atccctggag aacagtataa 180  
aaatggatta tcttgagatg ggtttatgta taataattaa taataagaat ttctataaaa 240

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<210> 202  
<211> 277  
<212> PRT  
<213> Homo sapiens

<400> 202

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20      25      30
Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
35      40      45
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50      55      60
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65      70      75
Leu Lys Tyr Glu Val Arg Asn Lys Asn Leu Thr Arg Glu Glu Ile
85      90      95
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100     105     110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115     120     125
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130     135     140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145     150     155
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
160     165     170
Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
175     180     185

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Phe Leu Tyr Ala Tyr Ser Thr Ala 200 Pro Gly Tyr Tyr Ser Trp Arg Asn  
195 205  
Ser Lys Asp Gly Ser Trp Phe Ile 210 Gln Ser Leu Cys Ala Met Leu Lys  
210 215 220  
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
225 230 235  
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
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His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu  
250 255  
Leu Tyr Phe Tyr His  
260 265 270 275

<210> 203  
<211> 1906  
<212> DNA  
<213> Homo sapiens

<400> 203  
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agcccaggcg agaggaaacg gctcccaggc aacttgttcc agcgtatgga tttctctcta 180  
gaacttcaga tacaagaaca aatggctatg tctggtgcac caggggggcaa aatcgataat 240  
tctgtgttag tctcttatgt gggcttatag acagtaggag ctggtgccta tgcctacaag 300  
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gaacagaaac agaaaaggcg cgcgttatct gcttcagaag gagaggaagt tcttcaagac 420  
aaggcgccaa gctatgttcc tttctgtcta attggtggag gcacagctgc ttttgcgtca 480  
gccagatcca gtccggctcg ggaatcctgg gccagggtac gtattgtatc tgaagatctc 540  
gagctgcctg acatgcgacc tctcttttca aaagaactgt ggttttcaga tgaccaccaat 600  
gtcacaaga cactgcgatt caaacagtgg aatggaaaag agagaagcat atatttcag 660  
ccacctctct tctatgtctc tgcctcaggac ctgcctcata ttgagaattg tgggtggct 720  
gtctctactg ggaagaaggt agtacacgtg gatgtgagag acaacatggt gaaacttaat 780  
gagggctctc aaataaccta tgaaaagtgc ttgattgcaa caggagggtac tccaagaagt 840  
ctgtctgcga ttgataggcg tggagcagag gtgaagagta gaacaacgtc tttcagaag 900  
attggagact ttagaagcct ggagaagatt tcacgggaag tcaaatcaat tacgatattc 960  
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ctattcaaca tcatgaaga ctgaagcccc acagtgaat ttgcaa 1906

<210> 204  
<211> 613  
<212> PRT  
<213> Homo sapiens

<400> 204  
Met Phe Arg Cys Gly Leu Ala Ala Gly Ala Leu Lys Gln Lys Leu  
1 5 10 15  
Val Pro Leu Val Arg Thr Val Cys Val Arg Ser Pro Arg Gln Arg Asn  
20 25 30  
Arg Leu Pro Gly Asn Leu Phe Gln Arg Trp His Val Pro Leu Glu Leu  
35 40 45  
Gln Met Thr Arg Gln Met Ala Ser Ser Gly Ala Ser Gly Gly Lys Ile  
50 55 60  
Asp Asn Ser Val Leu Val Leu Ile Val Gly Leu Ser Thr Val Gly Ala  
65 70 75 80

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Gly Ala Tyr Ala Tyr Lys Thr Met Lys Glu Asp Glu Lys Arg Tyr Asn  
 85 90 95  
 Glu Arg Ile Ser Gly Leu Gly Leu Thr Pro Glu Gln Lys Gln Lys Lys  
 100 105 110  
 Ala Ala Leu Ser Ala Ser Glu Gly Glu Val Pro Gln Asp Lys Ala  
 115 120 125  
 Pro Ser His Val Pro Phe Leu Ile Gly Gly Gly Thr Ala Ala Phe  
 130 135 140  
 Ala Ala Ala Arg Ser Ile Arg Ala Arg Asp Pro Gly Ala Arg Val Leu  
 145 150 155  
 Ile Val Ser Glu Asp Pro Glu Leu Pro Tyr Met Arg Pro Pro Leu Ser  
 160 165 170 175  
 Lys Glu Leu Trp Phe Ser Asp Asp Pro Asn Val Thr Lys Thr Arg  
 180 185 190  
 Phe Lys Gln Trp Asn Gly Lys Glu Arg Ser Ile Tyr Phe Gln Pro Pro  
 195 200 205  
 Ser Phe Tyr Val Ser Ala Gln Asp Leu Pro His Ile Glu Asn Gly Gly  
 210 215 220  
 Val Ala Val Leu Thr Gly Lys Lys Val Val Gln Leu Asp Val Arg Asp  
 225 230 235 240  
 Asn Met Val Lys Leu Asn Asp Gly Ser Gln Ile Thr Tyr Glu Lys Cys  
 245 250 255  
 Leu Ile Ala Thr Gly Gly Thr Pro Arg Ser Leu Ser Ala Ile Asp Arg  
 260 265 270  
 Ala Gly Ala Glu Val Lys Ser Arg Thr Thr Leu Phe Arg Lys Ile Gly  
 275 280 285  
 Asp Phe Arg Ser Leu Glu Lys Ile Ser Arg Glu Val Lys Ser Ile Thr  
 290 295 300  
 Ile Ile Gly Gly Gly Phe Leu Gly Ser Glu Leu Ala Cys Ala Leu Gly  
 305 310 315 320  
 Arg Lys Ala Arg Ala Leu Gly Thr Glu Val Ile Gln Leu Phe Pro Glu  
 325 330 335  
 Lys Gly Asn Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr  
 340 345 350  
 Met Glu Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile  
 355 360 365  
 Val Gln Ser Val Gly Val Ser Ser Gly Lys Leu Leu Ile Lys Leu Lys  
 370 375 380  
 Asp Gly Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu  
 385 390 395 400  
 Glu Pro Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser  
 405 410 415  
 Asp Phe Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn  
 420 425 430  
 Ile Trp Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly  
 435 440 445  
 Arg Arg Arg Val Glu His His Asp His Ala Val Val Ser Gly Arg Leu  
 450 455 460  
 Ala Gly Glu Asn Met Thr Gly Ala Ala Lys Pro Tyr Trp His Gln Ser  
 465 470 475 480  
 Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly Tyr Glu Ala Ile Gly  
 485 490 495  
 Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val Phe Ala Lys Ala Thr  
 500 505 510  
 Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln Ser Gly Thr Gly Ile  
 515 520 525  
 Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser Val Ile Thr Ile Pro  
 530 535 540  
 Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val Gln Gly Glu Asp Tyr  
 545 550 555 560  
 Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys Val Val Val Gly Ile  
 565 570 575  
 Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile Ala Arg Lys Ile Ile  
 580 585 590  
 Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu Val Ala Leu Phe  
 595 600 605  
 Asn Ile His Glu Asp  
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<210> 205
<211> 1090
<212> DNA
<213> Homo sapiens

<400> 205
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gaactctctc tggagaaagg catcatcacc ttggaaatga gggagctcat ccaggccaaa 180
gtgggcagtt tcagccagaa tttggaactc ctcaacttgc tgccaaagag ggttcccaaa 240
gcttttgatg cttccttgga agccttgcac tcttgaattt tatcaaacac acttccagct 300
ggcatatagg ttgcagcttc ggctctgtgg cctagcactg gtgttgagca atgtgcactt 360
cactggagag aaagaactgg aatttcgttc tggaggggat gtggaccaca gtactctagt 420
caccctcttc aagcttttgg gctatgacgt ccatgttcta tgtgaccaga ctgcacagga 480
aatgcaagag aaactgcaga attttgcaca gttactctga caccgagtca cgactgtctg 540
catctgtgca ctctctctgc atggtgtgga gggcgcctac tatgtgtggt atgggaaact 600
gtctccagctc caagagggttt ttcagctctt tgacaacgcc aaccgcccaa gcctacagaa 660
caaaccaaaa atgtttctta tccagccctg ccgtggagat gagactaatc gtgggggtga 720
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gaagcagctt atcaaggatc gggaaggtaa tgctctgggc acagaatttc accggtgcaa 1020
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tcccacatga                                     1090

<210> 206
<211> 91
<212> PRT
<213> Homo sapiens

<400> 206
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Pro His His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala Lys
20 25 30
Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp Ile
35 40 45
Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly Ser Phe
50 55 60
Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro Gln
65 70 75 80
Ala Phe Asp Ala Phe Cys Glu Ala Leu His Ser
85 90

<210> 207
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 207
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gaactctctg ggggaccgtc agtcttctctc ttccccccaa aaccacaaga caccctcatg 120
atctcccgga cccctgaggt cacatgcgtg gtgggtgacg tgagccacga agacctgtag 180
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tggctgtaag gcaaggagta caagtgtcaag gtctccaaca aagccctccc agccccctac 360
gagaaaaaaa tctccaaagc caaagggcag ccccgagacg cacagtgtta caccctgcc 420
catcccgagg atgagctgac caagaaccag gtccagccta cctgctctgt caaagcttc 480
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accacgcctc ccgtgtctga ctccgacggc tctcttcttc tctacagcaa gctcacctgt 600
gacaaagaca ggtgtcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 660
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatgatc taga 714

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<210> 208  
<211> 235  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 208  
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20 25 30  
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
35 40 45  
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
50 55 60  
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
65 70 75 80  
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
85 90 95  
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
100 105 110  
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
115 120 125  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
130 135 140  
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Lys Val Lys Gly Phe  
145 150 155 160  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
165 170 175  
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
180 185 190  
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
195 200 205  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
210 215 220  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230 235

<210> 209  
<211> 718  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<221> misc\_feature  
<222> 34, 43, 52, 55, 58, 64  
<223> n = A,T,C or G

<400> 209  
tgatcaagaa ccacatggag gatgcacgtg ccncagtgcc ccncaatgcc cngcncnnga 60  
actncaagga ggcctctctg tctttgtctt ccccccgaaa cccaaggagc tcctctccat 120  
ttttggaggg cgagtcacgt gcgttgtagt ggcagctcga aagaagagacc ccgaggtcaa 180  
tttcaactgg tatattgatg gcgttgaggt ggcgaacggc caaagagga 240  
acagttcaac agcagctacc gcgtgggtcag cgtctgccc atccagcacc aggactggct 300  
gacggggaag gaattcaagt gcaagggtcaa caaaaagct ctcccggccc ccactcgagag 360  
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ccgggaagaa ctggccaagg acaccgtagc cgtaacatgc ctggtcaaaag gcttctaccc 480  
agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc 540  
caacacgcgc ccacagctgg acaacgacgg gacctaactc ctctacagca agctctcggt 600  
gggaaagaac acgtggcagc ggggagaaac cttaacctgt gtggtgatgc atgaggccct 660  
gcacaaccac tacaccaga aatccatcac ccagctctcg ggtaaatagt aatctaga 718

<210> 210  
<211> 757

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<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 210

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catcttcccc	ccgaaaccca	aggagctcct	ctccatttct	gggagggccg	aggctacggt	180
cgctgtggta	gacgtgggcc	agggaagacc	cgaggtcagt	ttcaactggt	acattgatgg	240
cgctgaggtg	cgacgggcca	acacgagggc	aaaagaggaa	cagttcaaca	gcacgtaccg	300
cggtggtcag	gtcttgccca	tccagcacca	ggactggctg	acgggggaagg	aattcaagtg	360
caaggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accactctca	aggccaaagg	420
cgagaccggg	gagccgcagg	tgtaaccctt	ggcccaaac	cggggaagagc	tggccaagga	480
caccgtgagc	gtaacatgcc	tggtcaaaag	cttctaccca	cttgatatca	acgttgagtg	540
cgagaggaa	gggcagccgg	agtcagaggg	cacytacgcc	accagcccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	ggaagaagaa	cggtggcagca	660
gggagaagcc	ttcactgtgt	tggtgatgca	cgaggccctg	cacaaccact	acaccagaa	720
atccatcacc	cagtcttcgg	gtaaatagta	atctaga			757

<210> 211

<211> 727

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 211

tgatcaagcg	caccacagcg	aagaccgccg	ctccaagtgt	cccaaatgcc	caggccctga	60
actccttgga	gggcccacg	tcttcatctt	cccccgaaa	gccaaaggag	tctctccat	120
cacccgaaaa	cttgaggtca	cgctcttggt	gtggagctgg	gtaaaagaa	ccctgagatc	180
gagttcaagc	tggtccgtgg	atgacacaga	ggtacacacg	gctgagacaa	agccaaagga	240
ggaacagttc	aacagcagct	accgcgtggt	cagcttctgt	ccatccagc	accaggactg	300
gctgacgggg	aaggaaattca	agtgcgaagt	caacaacaaa	gctctccagc	cccccatcga	360
gaggaccatc	tccaaggcca	aagggcagac	ccgggagccg	caggtgtaca	ccctggcccc	420
acaccgggaa	gagctggcca	aggacacgt	gagcgtaacc	tgccctgtga	aaggcttctt	480
cccagctgac	atcaacggtg	agtggcagag	gaatgggcag	ccggagtcag	agggcaccta	540
cgcccaacac	ccgcacacag	tggaacaaga	cgggaccctac	ttctcttaca	gcaaacctctc	600
cgtagggaaa	aacacgtggc	agcaggggaga	agtccttcacc	tgtgtggtga	tgacagaggc	660
tctacacaat	cactccacc	agaaatccat	caccagctct	tcgggtaaat	agtaactctag	720
agggccc						727

<210> 212

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 212

Glu	Pro	His	Gly	Gly	Cys	Thr	Cys	Pro	Gln	Cys	Pro	Ala	Pro	Glu	Leu
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Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
			20						25					30	
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
			35						40				45		
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
			50				55				60				
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser
					70					75				80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
					85				90					95	
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
			100				105						110		
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
			115				120				125				

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr  
 130 135 140  
 Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn  
 145 150 155 160  
 Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala  
 165 170 175  
 Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser  
 180 185 190  
 Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr  
 195 200 205  
 Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 210 215 220  
 Ile Thr Gln Ser Ser Gly Lys  
 225 230

<210> 213  
 <211> 248  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion polypeptide

<400> 213  
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 1 10 15  
 Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu  
 20 25 30  
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp  
 35 40 45  
 Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp  
 50 55 60  
 Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly  
 65 70 75 80  
 Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn  
 85 90 95  
 Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp  
 100 105 110  
 Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro  
 115 120 125  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu  
 130 135 140  
 Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp  
 145 150 155 160  
 Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile  
 165 170 175  
 Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr  
 180 185 190  
 Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr  
 195 200 205  
 Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe  
 210 215 220  
 Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 225 230 235 240  
 Ser Ile Thr Gln Ser Ser Gly Lys  
 245

<210> 214  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion polypeptide

<400> 214  
 Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys

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 1 5 10 15  
 Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro  
 20 25 30  
 Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys  
 35 40 45  
 Leu Trp Trp Thr Trp Val Lys Thr Leu Arg Ser Ser Ser Ser Trp  
 50 55 60  
 Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu  
 65 70 75  
 Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln  
 80 85 90  
 His Gln Asp Trp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn  
 95 100 105  
 Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly  
 110 115 120  
 Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu  
 125 130 135  
 Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe  
 140 145 150  
 Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser  
 155 160 165  
 Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr  
 170 175 180  
 Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln  
 185 190 195  
 Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His  
 200 205 210  
 Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys  
 215 220 225 230 235

<210> 215

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Fusion polynucleotide

<400> 215

gatcaggagc ccaaatcttg tgacaaaact cacacatgcc caccggtgcc agca 54

<210> 216

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Fusion polypeptide

<400> 216

Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 1 5 10 15  
 Pro Ala

<210> 217

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Fusion polynucleotide

<400> 217

gatctggagc ccaaatcttg tgacaaaact cacacatgcc caccggtgcc agca 54

<210> 218

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 218  
Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
1 5 10 15  
Pro Ala

<210> 219  
<211> 327  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 219  
cctgaactcc tggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 60  
atgatctccc ggaccctcga ggtcacatgc gtggtggtgg acgtgagcca cgaagacctc 120  
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataaagccaa gacaaagccg 180  
cgggaggagc agtacaacag cagctaccgt gtggtcagcg tctctaccgt cctgcaccag 240  
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 300  
atcgagaaaa ccattctcaa agccaaa 327

<210> 220  
<211> 109  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 220  
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
1 5 10 15  
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
20 25 30  
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
35 40 45  
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Glu  
50 55 60  
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Glu  
65 70 75 80  
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
85 90 95  
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
100 105

<210> 221  
<211> 324  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 221  
gggcagctcc gagaaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 60  
aaccaagctca gcttgaccty cctggtcaaa ggcttctatc ccagcgacat cgcctggag 120  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcttcccggt gctggactcc 180  
gacggctctt tcttctctta tagcaagctc accgtggaca agagcagggt gcagcagggt 240  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accattacac gcagaagagc 300

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt 324

ctctccctgt ccccggttaa atga

<210> 222  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 222  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
1 5 10  
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
20 25 30  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
35 40 45  
Asn Asn Tyr Ser Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
50 55 60  
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
65 70 75 80  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
85 90 95  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 223  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 223  
gatcaggagc ccaatcttc tgacaaaact cacacatccc caccgtcccc agca 54

<210> 224  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 224  
Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser  
1 5 10 15  
Pro Ala

<210> 225  
<211> 712  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 225  
tgatcacccc aaatcttctg acaaaactca cacatctcca cgtcctcag cactgaact 60  
ctcgggtgga cgtcagttc tcctcttccc cccaaaacc aaggacacc tcattgatctc 120  
cggaccctt gaggtcacat gcgtggtggt ggacgtgagc cactgaagacc ctgagggtcaa 180  
gttcaactgg tacgtggagc gcgtggaggt gcataatgcc aagacaagc cgcgggagga 240

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gcagtaaac agcacgtacc gtgtggtcag cgtcttcacc gtctgcacc aggactggct 300  
gaatggcaag gagtacaagt gcaaggcttc caacaaagcc ctccagccc ccactgagaa 360  
aacaattctcc aaagccaaag ggcagccccc agaaccacag gtgtacaccc tgcccccatc 420  
ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctggtcaaat gcttctatcc 480  
cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac 540  
gcctcccggt ctggactccg acgctctctt ctctctctac agcaagctca ccgtggacaa 600  
gagcaggtgg cagcagggga acgtctcttc atgctccgtg atgcatgagg cctgcacaa 660  
ccactacacg cagaagagcc tctccctgtc tccgggtaaa tgataatcta ga 712

<210> 226  
<211> 233  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 226  
Asp His Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser  
1 5 10 15  
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
20 25 30  
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
35 40 45  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
50 55 60  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
65 70 75 80  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
85 90 95  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
100 105 110  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
115 120 125  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
130 135 140  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
145 150 155  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
160 165 170  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
175 180 185 190  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220  
Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 227  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' primer for llama IgG1 constant region

<400> 227  
gttgttgatc aagaaccaca tggaggatgc acgtg

35

<210> 228  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> 5' primer for llama ig2 constant region

<400> 228  
gtgtgtgatac aagaacccaa gacacaaaa cc 32

<210> 229  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' primer for llama IgG3 constant region

<400> 229  
gtgtgtgatac aagcgacca cagcgaagac ccc 33

<210> 230  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Llama Fc sense sequencing primer

<400> 230  
ctgagatcga gtccagctg 19

<210> 231  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Llama Fc antisense sequencing primer

<400> 231  
cctcctttgg ctttgtctc 19

<210> 232  
<211> 1527  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<221> misc\_feature  
<222> 843, 852, 861, 864, 867, 873  
<223> n = A,T,C or G

<400> 232  
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgcttca 60  
gtcataattg ccagaggaca aattgtcttc tccagctctc cagcaatcct gtcctgcatct 120  
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcatctgg 180  
taccagcaga agccaggatc ctccccaaa cctctggattt atgcccctac caacctggct 240  
tcctggattcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcaaatc 300  
agcagagtgg aggcctgaaga tgcctgccat tattactgcc agcagttggag ttttaaccaca 360  
ccacagctcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
agggcctgggg ctctcagtga gatgtcctgc aaggcctctg gctacacatt taccagttac 540  
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctgacagcgc tgacatctga agactctgctg 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cagatgtctgg 780  
ggcacaggga ccacggctac cgtctcttct gatcaagaac cacatggagg atgcacgtgc 840

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 ccnagctgccc cnaaatgccc ngcncngaa ctncaggag gcccttctgt crrtgtcttc 900  
 ccccggaac ccaaggagct cctctccatt ttggaggcc gagtcacgt cgttgtagtg 960  
 cagctcgga aagaagacc cgaggtcaat ttcaactggt atattgatgt cgttgagggt 1020  
 cgaagggcca atacgaagcc aaaaggagaa cagttcaaca gcacgtaccg cgttgtcagc 1080  
 gtctcgccc tccagacca ggaactggctg acggggaagg aattcaagtg caaggtcaac 1140  
 aacaagagctc tcccgcccc catcgagagg accattccca aggcacaagg gcagaccggt 1200  
 gagcgcaggg tgtacacct ggcgccacac cgggaagaac cgtgacatca acggtgagtg 1260  
 gtaacatgct tgttcaaaag cttctaccaca cacttacgccc aacacgcgcg gcagctgagc 1320  
 ggtcagcgcg agtcagagga gctcactggg ggaagagaaa cgtggcagcg gggagaaacc 1380  
 acctacttcc tctcagacaa gtctcctggg ggaagagaaa cgtggcagcg gggagaaacc 1440  
 ttaacctgtg tgggtatgca tgaggcctgt acaccagaa atccatcacc 1500  
 cagctctcgg gtaaatagta atctaga cacaaccat acaccagaa atccatcacc 1527

<210> 233  
 <211> 1566  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 233  
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtctca 60  
 gtcataattg ccagaggaca aattgttctc tcccagcttc cagcaatcct gcttgcatct 120  
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcatcgg 180  
 taccagcaga agccaggatc ctcccccaaa ccttgatttt atgcccctac caactctggt 240  
 tctggagctc ctgctgcctt cagtggcagt gggctcgga cctcttacct tctcacaatt 300  
 agcagagtcg aggtcgaaga tgctgccact tattactgcc agcagtgagg ttttaaccac 360  
 cccacgttgc gtctgggac caagctggag cgttgagctc gcggtggctc gggcggtggt 420  
 ggaactggag gagggtggag ctctcaggct tatctacagc agtctggggc tgagctgtgt 480  
 aggcctgggg ctctagttaa gatgtctctg aaggcttctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggctcgg aatggattgg agctatttat 600  
 ccaggaaatg gtataacttc ctacaatcag aagtccaagg atgactcgtg atgactcgtg 660  
 gacaattcct ccagcacagc ctacatgcag ctacagcagc tgacattctg agactctcgg 720  
 gtctatttct ggtgtactat agtaactctt actgttactt cgtatcttgg 780  
 ggccacaggga ccacggtcac cgtctcttct gatcaagaac ccaagacacc aaaaaccaaa 840  
 ccacaaccac aaccacaacc caatcctaca acagaattca agtgctccaa atgtccacca 900  
 cctgagctcc tggggaggcc ctacgtcttc atcttctccc cgaaccacca ggacgtcttc 960  
 tccatttctg ggaagcccca ggtcacgtgc gctgagtgcc gactggccat cagcagcc 1020  
 gaggtcagtt tcaacttgta cattgatggc gttggtcagc aaggtcaaca cagcagcc 1080  
 aagaaggaa agttcaacag acgtacacgc aggtgacac aaggtcagc cagcagcc 1140  
 gactggctga cggggaagga attcaagtg cagaccagc agccacaggt gtacaccctg 1200  
 atcgaagaa ccatctccaa ggccaaaggc cagaccggg agccacaggt gtacaccctg 1260  
 gcccacacc gggaagagct cggcaaggac acctgagcg acctgagcg taacatgctt ttttaaccac 1320  
 tttaccacc ctgatataaa cgttgagtg cagaagaatg ggcagccgga gtcagagg 1380  
 acytaccca ccacgccacc ctagctggac aacgacggga ctaactctct ctacagcagg 1440  
 ctctcgggtg gaagaacac gtggcagcag ggagaaacct tcaactctgt ggtgatgac 1500  
 gaggcctgc acaccacta caccagaaa tccatcacc agtctcggg taaatagtaa 1566  
 tctaga

<210> 234  
 <211> 1536  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 234  
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtctca 60  
 gtcataattg ccagaggaca aattgttctc tcccagcttc cagcaatcct gcttgcatct 120  
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcatcgg 180  
 taccagcaga agccaggatc ctcccccaaa ccttgatttt atgcccctac caactctggt 240  
 tctggagctc ctgctgcctt cagtggcagt gggctcgga cctcttacct tctcacaatt 300  
 agcagagtcg aggtcgaaga tgctgccact tattactgcc agcagtgagg ttttaaccac 360  
 cccacgttgc gtctgggac caagctggag cgttgagctc gcggtggctc gggcggtggt 420  
 ggtcagcgcg aggttggagg ctctcaggct tatctacagc agtctggggc tgagctgtgt 480  
 aggcctgggg ctctagttaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga aatggattgg agctatttat 600

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 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctacagcagg tgacatctga agactcttgcg 720  
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actgtgtactt cgtgtctgg 780  
 ggccagaggga ccacggtcac cgtctcttct gatcaagcga accacagcga agacccagc 840  
 tccaagtgtc ccaaatgccg agggcctgaa ctcttggag ggccacggt ctctatcttc 900  
 cccccgaag ccaaggacgt cctctccatc acccgaaaac ctgaggctac gtgcttgg 960  
 tggacgtggg taaagaagac cctgagatcg agttcaagct ggtcgtgga tgacacagag 1020  
 gtacacacgg ctgagacaaa gccaaaaggag gaacagtcca acagcacgta ccgctgggtc 1080  
 agcgtctctgc cctccagca ccaggactgg ctgacgggga aggaattcaa gtgcaaggct 1140  
 aacaacaaag cctctccagc cccatccgag aggcactct ccaaggccaa agggcagacc 1200  
 cggggagcgc aggtgtcac cctggcccca cccggggaag agctggccaa ggacaccgtg 1260  
 agcgttaacc cctgtgtcac aggtctcttc ccagctgaca tcaacgttga gtggcagagg 1320  
 aatgggcagc cggagtcaga gggcactcac gccaacagc gcgcacagct ggacaacgac 1380  
 gggacctact tctctacag caaactcttc gtgggaaga acacgtggca gcagggagaa 1440  
 gtcttcacct gtgtgtgat gcacgaggct ctacacaatc actccacca gaaatccatc 1500  
 accagctctt cgggtaata gtaatctaga gggccc 1536

<210> 235  
 <211> 498  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 235  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro His Gly  
 260 265 270  
 Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu Pro Gly Gly Pro  
 275 280 285  
 Ser Val Phe Val Phe Pro Pro Lys Asp Val Leu Ser Ile Phe  
 290 295 300  
 Gly Gly Arg Val Thr Cys Val Val Val Asp Val Gly Lys Lys Asp Pro  
 305 310 315 320  
 Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val Glu Val Arg Thr Ala  
 325 330 335  
 Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 340 345 350  
 Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe  
 355 360 365  
 Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr  
 370 375 380  
 Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu  
 385 390 400  
 Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys  
 405 410 415  
 Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn Val Glu Trp Gln Arg  
 420 425 430  
 Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln  
 435 440 445  
 Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly  
 450 455 460  
 Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr Cys Val Val Met His  
 465 470 475 480  
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser  
 485 490 495  
 Gly Lys

<210> 236

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 236

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Thr  
 260 265 270  
 Pro Lys Pro Gln Pro Gln Pro Gln Pro Asn Pro Thr Thr Glu  
 275 280 285  
 Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

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290 295 300

Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Ser Ile Ser Gly  
305 310 320

Arg Pro Glu Val Thr Cys Val Val Val Asp Val Gly Gln Glu Asp Pro  
325 335

Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly Ala Glu Val Arg Thr Ala  
340 350

Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val  
355 365

Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe  
370 380

Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
385 390 400

Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu  
405 415

Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys  
420 430

Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile Asn Val Glu Trp Gln Arg  
435 445

Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Thr Thr Pro Pro Gln  
450 455

Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly  
465 470 480

Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe Thr Cys Val Val Met His  
485 495

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser  
500 505 510

Gly Lys

<210> 237  
<211> 503  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 237

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125

Asp Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
225 230 235 240  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Ala His Ser His  
260 270  
Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys Pro Gly Pro Glu Leu  
275 285  
Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro Lys Ala Lys Asp Val  
290 295 300  
Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys Leu Trp Trp Thr Trp  
305 310 315 320  
Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp Ser Val Asp Asp Thr  
325 335  
Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser  
340 350  
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Asp Trp Leu  
355 365  
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala  
370 375 380  
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro  
385 390 395 400  
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr  
405 410 415  
Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe Pro Ala Asp Ile Asn  
420 425 430  
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala  
435 440 445  
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser  
450 455 460  
Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Val Phe Thr  
465 470 475 480  
Cys Val Val Met His Glu Ala Leu His Asn His Ser Thr Gln Lys Ser  
485 490 495  
Ile Thr Gln Ser Ser Gly Lys  
500

<210> 238

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-primer for llama IgG1, IgG2, IgG3 constant region

<400> 238

gtgttttcta gattactatt taccgaaga ctgggtgatg ga

42

<210> 239

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 239

aagcttgccg ccatggattt tcaagtgcag attttcagct tctcgtact cagtgttca 60  
gtcataattg ccaggaggaca aattgttctc tccagctctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactctg 180  
taccagcaga agccaggatc ctcccccaaa cctctgattt atgccccatc caacctggct 240  
tctggagttc ctgctgcctt cagtggcagt gggctggga cctcttactc tctcacaatc 300  
agcagagtgg aggcctaaga tgcctgcact tattactgcc agcagtggag tttaaccaca 360  
ccacgtttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgg 420  
ggactctggg gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480  
aggctggggg cctcagtgaa gatgtctctg aaggctctcg gctacacatt taccagttac 540  
aatagcactt gggtaaaaca gacacctaga cagggctctg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagtcaagg gcaaggccac actgactgta 660

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gacaaatccct ccagcacagc ctacatgcag ctacagcagcc tgacatctga agactctgcg 720  
gtctatttct gtgcagaggt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaatcttg tgacaaaact 840  
cacacatgcc caccgtgccc agcacctgaa ctctctgggg gaccgtcagt ctctctcttc 900  
ccccaaaac ccaaggacac cctcatgac tcctcgacc ctgaggtcac atgctgtgtg 960  
gtggacgtga gccacgaaga ccttgaggtc aagtccaact ggtacgtgga cggcgtggag 1020  
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgttc 1080  
agcgtctctca cgtctctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140  
tccacaaga cctctccagc cccatcgag aaaacaatct ccaaagccaa agggcagccc 1200  
cgagaaccac aggtgttacac cctgccccc tcccggtgat agctgaccaa gaaccaggtc 1260  
agcctgacct gccctgtcaa aggcctctat cccagcgaca tcgctgtgga gtgggagagc 1320  
aatgggcagc cggagaaacaa ctacaagacc acgcctcccg tctgtgagtc cgacggcttc 1380  
ttctctctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgctctc 1440  
tcagtctcgc tgatgcagga ggctctgcac aaccactaca cgcagaagag cctctctctg 1500  
tctccgggta aatgactag a 1521

<210> 240

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 240

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser  
260 265 270  
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
275 280 285  
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
290 295 300  
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
305 310 315 320  
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
325 330 335  
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
340 345 350

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
355 360 365  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Asp Pro Ala Pro  
370 375 380  
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
385 390 395 400  
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
405 415  
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
420 430  
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
435 440 445  
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
450 455 460  
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
465 470 475 480  
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
485 490 495  
Ser Pro Gly Lys  
500

<210> 241  
<211> 162  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 241  
gcgagtcctt cgaacctgct cccatctcgg gccattacct taatctcagt aaatggaatt 60  
tttgatgat gctgcctgac ctactgcttt gccccaagat gcagagagag aaggaggaat 120  
gagagattga gaaggggaag tgtacgccct gtataatcgt at 162

<210> 242  
<211> 51  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 242  
Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser  
1 5 10 15  
Val Asn Gly Ile Phe Val Ile Cys Lys Leu Thr Tyr Cys Phe Ala Pro  
20 25 30  
Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val  
35 40 45  
Arg pro Val  
50

<210> 243  
<211> 399  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 243  
aagcttatgg attttcaagt gcagattttc agcttctcgc taatcagtc ttcagtcata 60  
atgtccagag gagtgcagat tgttctgact cagtctccag ccacctgtc tgtgactcca 120  
ggagatagag ttctcttttc ctgcagggcc agccaagta ttacgacta cttaactgg 180  
ttcaacaaca aatcacatga gtctccaagg ctctcatca aatatgtctc ccattccatc 240  
tctgggatcc ctctcagggt cagtggcagt ggcacagggt cagatttcac tctcagatc 300  
aacagtgtgg aacctgaaga tgttggaaat tattactgtc aacatgggtc cagctttccg 360

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
tggacgttcg gtggaggcac caagctggaa atcaaacgg 399

<210> 244  
<211> 131  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 244  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala  
35 40 45  
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His  
50 55 60  
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly  
65 70 75  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu  
80 85 90  
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln  
100 105 110  
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg  
130

<210> 245  
<211> 368  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 245  
cagatccagt tgggtgcaatc tggacctgag ctgaagaagc ctggagagac agtcaggatc 60  
tcctgcaagg ctctgggta tgccttcaca actactggaa tgcagtgggt gcaagagatg 120  
caggaaaggt gtttgaagt gattggctgg ataaacacc cactctggag tgccaaata 180  
tgtagaagac ttcaaggacg gtttgccttc tctttggaaa cctctgccaa cactgcata 240  
ttacagataa gcaacctcaa agatgaggac acggctacgt attctgtgt gagatccggg 300  
aatgttaact atgacctggc ctactttgct tactggggcc aagggacact ggtcactgtc 360  
tctgatca 368

<210> 246  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 246  
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15  
Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Thr  
20 25 30  
Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile  
35 40 45  
Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu  
50 55 60  
Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr  
65 70 75  
Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys  
80 85 90 95

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp  
100 105 110  
Gly Gln Gly Thr Leu Val Thr Val Ser  
115 120

<210> 247  
<211> 812  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> fusion polynucleotide

<400> 247  
aagcttatgg attttcaagt cgagattttc agcttctcgc taatcagtcg ttcagtcata 60  
atgtccagag gagtgcacat tgttctgact cagtctccag ccacctgtc tgtgactcca 120  
ggagatagag tctctctttc ctgcagggcc agccagagta ttacgcacta cttacactgg 180  
tatcaacaaa aatcacatga gtctcccaagg ctctctcatca aatatgtctc ccattccatc 240  
tctgggattcc cctccaggtt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300  
aacagtgtgg aacctgaaga tgttggaaatt tattactgtc aacatgtgta cagctttccg 360  
tggagcttctg gtggaggcac caagctggaa atcaaacggg gtggcggtgg ctggggcgga 420  
gggtgggtcgg gtggcggtgg atctcagatc cagttgtgtg aatctggacc tgagctgaag 480  
aagctctggag agacagtcag gatctctctg aaggcttctg ggtatgcctt cacaactact 540  
ggaaatgcagt ggggtgcaaga gatgccagga aagggtttga agtggattgg ctggataaac 600  
accctactct ggagtgccaa aatatgtaga agacttcaag gacgggtttg ctctctcttg 660  
gaaacctctg ccaactatgc atattacag ataagcaacc tcaaagatga ggacacggct 720  
acgtatttct gtgtgagatc cgggaatggt aactatgacc tggcctactt tgcttactgg 780  
ggccaaggga cactggtcac tgtctctgat ca 812

<210> 248  
<211> 267  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> fusion polypeptide

<400> 248  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala  
35 40 45  
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His  
50 55 60  
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu  
85 90 95  
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln  
100 105 110  
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro  
145 150 155 160  
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr  
165 170 175  
Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys  
180 185 190  
Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg  
195 200 205  
Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr  
210 215 220  
Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Gly Asp Thr Ala Thr Tyr  
225 230 235 240

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala  
245 250 255  
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
260 265

<210> 249  
<211> 405  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 249  
atggattttc aagtgcagat tttcagcttc ctgctaatac gtgcttcagt cataatgtcc 60  
agaggagtcg acattgtgct caccacaatc ccagcttctt tggctgtgct tctaggtcag 120  
agagccacca tctcttgca ggcagtgaa agtgttgaa attatgtcac aagtttaagt 180  
cagtggtacc aacagaaacc aggcagacca ccaaaactcc tcattcttcg tgcattcaac 240  
gtagaatctg ggggtccctg caggtttagt ggcagtgagg ctgggacaga cttcagcttc 300  
aacatccatc ctgtggagga ggaatgatatt gcaatgtatt tctgtcagca aagtaggaag 360  
gttctctgga cgttcgggtg aggcaccaag ctggaaatca aatcg 405

<210> 250  
<211> 135  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 250  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala  
35 40 45  
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln  
50 55 60  
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn  
65 70 75  
Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr  
80 85 90 95  
Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met  
100 105 110  
Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly  
115 120 125  
Thr Lys Leu Glu Ile Lys Arg  
130 135

<210> 251  
<211> 369  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 251  
cagggtgcagc tgaaggagtc aggcactggc ctggtggcgc cctcacagag cctgtccatc 60  
acatgcacgc tctcagggtt ctcatcaacc ggctatgggt taaactgggt tcgccagcct 120  
caggaaagggt gctcggagtg gctgggaatg atatgggggt atggaagcac agactataat 180  
tcagctctca aatccagact gagcatcacc aaggacacct ccaagagcca agtttctta 240  
aaaatgaaca gtcgtcaaac tgatgacaca gccagatact actgtgccag agatgggtat 300  
agtaactctc attactatgt tatggactac tggggctcaag gaacctcagt caccgtctcc 360  
tcagatctgt

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 252  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 252  
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln  
1 5 10 15  
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr  
20 25 30  
Gly Val Asn Trp Val Arg Gln Pro Gly Lys Gly Leu Trp Leu  
35 40 45  
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys  
50 55 60  
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu  
65 70 75  
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala  
85 90 95  
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly  
100 105 110  
Gln Gly Thr Ser Val Thr Val Ser  
115 120

<210> 253  
<211> 825  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 253  
aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtcg ttcagtcata 60  
atgtccagag gagtcgacat tgtgtctcacc caatctccag cttctttggc tgtgtctcta 120  
ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatatta tgtcacaagt 180  
ttaatgtagt ggtaccaaca gaaaccaggga cagccaccga aactctccat ctctgtgcca 240  
tccaagctag aatctggggg cctgtgccagg tttagtgcca gtgggtctgg gacagacttc 300  
agcctcaaca tccatcttgt ggaggagat gatatgcaa tgtattctg tcagcaaaagt 360  
aggaagggttc cttggacgtt cgggtgagcg accaagctgg aatcaaacg ggggtggcgt 420  
ggctcgggcg gaggtgggtc ggggtggcgc ggatctcagg tgcagctgaa ggaactcaga 480  
cctgtcctgg tggcgccctc acagagcctg tccatcacat gcacgctctc aggggtctca 540  
ttaaccggct atgggtgtaa ctgggttctgc cagcctccag gaaagggtct ggagtggctg 600  
ggaatgatat ggggtgatgg aagcacagac tataattcag ctctcaaatc cagactgagc 660  
atcaccaggg acaactccaa gagccaagtt ttcttaaaaa tgaacagctc gcaaacgtgat 720  
gcacacagcca gatactactg tgccagagat ggttatagta acttccatta ctatgttatg 780  
gactactggg gtcaaggaac ctccagtcacc gtctcctctg atcag 825

<210> 254  
<211> 271  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 254  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala  
35 40 45  
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln  
50 55 60  
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
65 Val Glu Ser Gly Val<sup>70</sup> Pro Ala Arg Phe<sup>75</sup> Ser Gly Ser Gly Ser Gly Thr<sup>80</sup>  
85  
Asp Phe Ser Leu Asn Ile His Pro Val<sup>90</sup> Glu Glu Asp Asp Ile Ala Met<sup>95</sup>  
100  
Tyr Phe Cys Gln Gln Ser Arg Lys Val<sup>105</sup> Pro Trp Thr Phe Gly Gly Gly<sup>110</sup>  
115  
Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly<sup>120</sup>  
130  
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys<sup>135</sup> Glu Ser Gly Pro Gly<sup>140</sup>  
145  
Leu Val Ala Pro Ser<sup>150</sup> Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly<sup>155</sup>  
160  
Phe Ser Leu Thr Gly Tyr Gly Val Asn<sup>165</sup> Trp Val Arg Gln Pro Pro Gly<sup>170</sup>  
180  
Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp<sup>185</sup>  
190  
Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser<sup>195</sup>  
200  
Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu<sup>205</sup> Thr Asp Asp Thr<sup>210</sup>  
215  
Ala Arg Tyr Tyr Cys<sup>220</sup> Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr<sup>225</sup>  
230  
Val Met Asp Tyr<sup>235</sup> Trp Gly Gln Gly Thr<sup>240</sup> Ser Val Thr Val Ser Ser<sup>245</sup>  
250  
260 265 270

<210> 255

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 255

atggattttc aagtgcagat tttcagcttc ctgctaatac gtgcttcagt cataatgtcc 60  
agaggagtcg acatccagat gacacagctc ccattccctac tgtctgcac tctgggaggc 120  
aaagtcacca tcacttgcaa ggcaagccaa gacattaaga agtatatagg ttggtaccaa 180  
cacaagcctg gaaaaggctc caggctgctc atatattaca catctacatt acagccaggc 240  
atcccatcaa ggttcagtcg aagttggctt gggagagatt attccctcag catcagaaac 300  
ctggagcctg aagatatagg aactattat tgtcaacagt atgataattc tccattgacg 360  
ttcggtctcg ggacaaagtt ggaataaaaa cgg 393

<210> 256

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 256

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5  
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser  
20 25 30  
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala  
35 40 45  
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly  
50 55 60  
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu  
85 90 95  
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu  
115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Ile Lys Arg  
130

<210> 257  
<211> 362  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 257  
gatgtacagc ttcaggagtc aggacctggc ctgctgaacc ctctcagtc tctgtctctc 60  
acctgctctg tcaactggcta ctccatcacc agtggtttct actggaactg gatccgacag 120  
tttccgggaa acaaaactgga atggatgggc cacataagcc acgacggtag gaataactac 180  
aacccatctc tcaataatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240  
ctgaagtiga gttctgtgac tactgaggac acagctacat atttctgtgc aagacactac 300  
ggtagtagcg gagctatgga ctactggggt caaggaaact cagtcaccgt ctctctgat 360  
ca 362

<210> 258  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 258  
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
1 5 10 15  
Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly  
20 25 30  
Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp  
35 40 45  
Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu  
50 55 60  
Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe  
65 70 75 80  
Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95  
Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Ser Val Thr Val Ser Ser  
115

<210> 259  
<211> 806  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 259  
aagcttatgg attttcaagt gcagattttc agcttctctg taatcagtc ttcagtcata 60  
atgtccagag gatcgacat ccagatgaca cagtcctcat cctcactgic tgcactctctg 120  
ggaggcaaaag tcacatcac ttgcaaggca agccaagaca ttaagaagta tataagttgg 180  
taccacacaca agcctggaaa aggtcccagg ctgctcatat attacacatc tacattacag 240  
caggcatccc acctcaagttt cagtggaaagt gggctctggga gagattattc cctcagcatc 300  
agaaaactgg agcctgaaga tattgcaact tattattgtc aacagtatga taattctcca 360  
ttgacgtttc gctcggggac aaagtgtgaa ataaaaacgg gtggcgttgg ctggggcgtt 420  
ggggggctgg gtggcggcgg atctgatgta cagcttcagg agtcaggacc tggcctctgt 480  
aaactctctc agtctctgtc tctcactctg tctgtcactg gctactccat caccagtggt 540  
tctcactgga actggatctg acagttttcg ggaacacaaac tgggaatggat gggccacata 600  
agccacgacg gtaggataaa ctacaacca tctctcataa atcgaattct catcactcgt 660  
gacacatcta agaaccagtt ttctctgaag ttgagttctg tgactactga ggacacagct 720

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
acatatttct gtgcaagaca ctacgtagt agcggagcta tggactactg gggtaagga 780  
acctcagtcac cgcgtctctc tgatca 806

<210> 260  
<211> 266  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 260  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser  
20 25 30  
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala  
35 40 45  
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Thr His Lys Pro Gly  
50 55 60  
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu  
85 90 95  
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro  
145 150 155 160  
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr  
165 170 175  
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu  
180 185 190  
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro  
195 200 205  
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
210 215 220  
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr  
225 230 235 240  
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly  
245 250 255  
Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
260 265

<210> 261  
<211> 417  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 261  
atggcatgga gctgcattat tttcttcttg gtatcagtaa ttacagggtg ccattcccgag 60  
gtcaagctgc agcagtcagg ttctgaacta gggaaacctg ggcctcagtg gaaactgtcc 120  
tgcaagactc caggctacat attcacagat cactatatatt ctggggtgaa acagaagcct 180  
ggagaaagcc tgcaagtggat aggaatgttt tatgggtggaa atggtgtgtac aagctacaat 240  
caaaaattcc agggcgaagg cacactgact gtatgataaaa tctctagcac agcctacaatg 300  
gaactcagca gccctgacatc tgaggattct gcatctatt actgtgcaag aaggccggtg 360  
gcgacgggac atgctatgga ctactggggg caggggatgc aagtattacgt ctctcca 417

<210> 262  
<211> 139  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> fusion polypeptide

<400> 262

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Met Ala Trp Ser Cys Ile Ile Phe Phe Leu Val Ser Val Ile Thr Gly
 1      5      10      15
Val His Ser Gln Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys
 20      25      30
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
 35      40      45
Thr Asp His Tyr Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu
 50      55      60
Gln Trp Ile Gly Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn
 65      70      75      80
Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser
 85      90      95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile
100      105      110
Tyr Tyr Cys Ala Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr
115      120      125
Trp Gly Gln Gly Ile Gln Val Thr Val Ser Ser
130      135
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<210> 263

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 263

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gacatagtgc tgactcagac tccagccact ctgtctcttaa ttccctggaga aagagtcaca 120
atgacctgtca agaccagtca gaatatattggc acaatctttac actggtatca ccaaaaacca 180
aaggaggcttc caagggtctt catcaagtat gcttcgcagc ccatctctgg gatccctccc 240
agattcagtg gcagtggttc ggaacacagat ttcactctca gcatcaataa cctggagcct 300
gatgatatcg gaattatta ctgtcaacaa agtagaagct ggcctgtcac gttcggctct 360
ggcaccaagc tggagataaa a
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<210> 264

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 264

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1      5      10      15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
 20      25      30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
 35      40      45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50      55      60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
 65      70      75      80
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85      90      95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100      105      110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
115      120      125
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 265  
<211> 1671  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

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<400> 265
aagcttatgg attttcaagt gcagattttc agcttctcgc taatcagtcg ttcagtcata 60
atgtccagag gagtcgacat tgttctgact cagctctccag ccacctgtgc tgtgactcca 120
ggagatagag tctctcttct ctgcagggcc agccagagta tttagcgacta ctacacatgg 180
tatcaacaaa aatcacatga gtctccaagg ctctctatca aatatgtcttc ccattccattc 240
tctgggatcc cctccagggt cagtggcaggt ggaatcagggt cagatttcac ttcagatattc 300
aacagtgtag aacctgaaga ttgtggaatt tattactgtc aacatgggtca cagctttccg 360
tggacgttct gtggaggcac caagctggaa atcaaacggg gtggcggtgtg ctggggcgga 420
ggtagggctcg gtggcgggcg atctcagatc cagttgtgtgc aatctggacc tgagctggaag 480
aagcctggag agacagtcag gatctcctgc aaggcttctg ggtagtgcctt cacaactact 540
ggaaatgcagt ggggtgcaaga gatgccaggga aagggttttga agtgatttgg ctggataaac 600
acccctactc tggagtgcctc aatatgtaga agacttcaag gacggtttgc ctctcttttg 660
gaaacctctg ccaacactgc atattttacag ataagcaacc tcaaaagatga ggacacgcgt 720
acgtatttct gtgtgagatc cgtgtgacac acttgaactc ctgggggggat tgcctactgg 780
ggccaaaggga cgtctccagg catgatctcc ttgacctctg aggtcacatg 840
acatcccccac agacacacct aggaagacct tgaagttcaag ctgcactgtt cctcttcccc 900
ccaaaaccca acgaagacct agcaagacct gcgggagggag cagtgacacg acgtggagcg 1020
gcagcttgacc cactgggtcac tgtctctgat ctggagccca aatcttctga caaaactcac 840
acatcccccac cgtctccagg catgatctcc ttgacctctg aggtcacatg 960
cgaagttgagc acgaagacct gcgggagggag cagtgacacg acgtggagcg 1020
cataatgcca agacaaagcc gcgggagggag aatggcaagg agtacaagtg caaagttcac 1080
gtcttcaccg tcttcgacca ggaatggctg atcgcaaaa accatttcca aagccaaagg gcagcccgga 1200
aacaaagccc tcccagcccc gaaccacagg tgatcacctt gcccccattc cgggatgagc tgaccaagaa ccaagtcagc 1260
gaaccacagg tgatcacctt ctctcatccc atcgacatcg ccgtggagtg ggaagagcaat 1320
ctgacctggc tggtaaaagg ctctcatccc agcgacatcg ccgtggagtg ggaagagcaat 1320
ggggacccgg agaacacata caagaccacg cctcccggtc tggactccga cggctctctc 1380
ttctcttaca gcaagctcac cgtggagcag agcaggtggc agcaggggaa cgtcttctca 1440
tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
ccgggtgaaag cggatctcttc gaacctgtct ccatctcctg ccatctcctg aatctcagta 1560
aatggaattt ttgtgatatg ctgcctgacc tactgtcttt ccccaagatg cacagagaga 1620
aggagaaatg agagatttag aagggaagt gtagcgcttg tataaatcga t 1671

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<210> 266  
<211> 552  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

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<400> 266
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
85 90 95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
145 150 155 160
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
165 170 175

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 Thr Thr Gly Met Gln Trp Val Gln Met Pro Gly Lys Gly Leu Lys  
 180 185 190  
 Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg  
 195 200 205  
 Arg Leu Gln Gly Arg Phe Ala Ser Leu Glu Thr Ser Ala Asn Thr  
 210 215 220  
 Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr  
 225 230 235 240  
 Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala  
 245 250 255 260  
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asp Leu Glu Pro Lys  
 260 265 270 275  
 Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu  
 275 280 285 290  
 Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 290 295 300 305  
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 305 310 315 320  
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
 325 330 335 340  
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser  
 340 345 350 355  
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 355 360 365 370  
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
 370 375 380 385  
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 385 390 395 400  
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln  
 400 405 410 415  
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 415 420 425 430  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 435 440 445 450  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 450 455 460 465  
 Thr Val Asp Lys Ser Asp Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 465 470 475 480  
 Val Met His Glu Ala Leu His Asn His Thr Gln Lys Ser Leu Ser  
 480 485 490 495  
 Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala  
 500 505 510 515  
 Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr  
 515 520 525 530  
 Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Asn Glu Arg Leu  
 530 535 540 545  
 Arg Arg Glu Ser Val Arg Pro Val  
 545 550

<210> 267  
 <211> 1683  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 267  
 aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtg c ttcagtcata 60  
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 ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatttta tgcacaaagt 180  
 tcaatgcagt ggtaccaca gaaaccagg gaaaccacca aactcctcat ctctgctgca 240  
 tccaaagtta aacttgggg ccttccagg tttatgggca gtgggtctgg gacagacttc 300  
 agcctcaaca tccatctgt gaggaggat gatattgc aa tatattctg tcagcaaatg 360  
 aggaaggttc ctgacgtt ggagggagg accaagctgg aaatcaaacg ggggtggcgt 420  
 ggtcggggcg gagggtggc gggtggcgg ggaattcagg tgcagctgaa ggaatcagg 480  
 ccttggcctg tggcgccctc acagagctg tccatccat gcacctctc aggttctcta 540  
 ttaaccgctg atggtgtaaa ctggttctgc cagcctccag gaaagggtct ggagtggtg 600

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 ggaatgatg ggggtgatg aagcacagac tataattcag ctctcaaatc cagactgagc 660  
 ataccacaag acaactccaa gagccaagtt ttcttaaaaa tgaacacgtc gcaactgatg 720  
 gacacagcca gatactactg tgccagagat ggttatagta actttcatta ctatgttatg 780  
 gactactggg gtaacaggaa ctcagtcacc gtctcctcag atctggagcc caaatcttct 840  
 gacaaaactc cccacatccc accgttcccc gacactgaac tcctgggggg tcctgcagtc 900  
 ttctctcttc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 960  
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 ggcgtggagg tgacataatg caagacaaga ccgctggagg agcagtacaa cagcagctac 1080  
 cgtgtgtgtc gcgtctctac cgtctctcac cctccagccc aaacattcga cgtgaccaa 1140  
 tgcaaggtct ccaacaagag ggtgtacacc ctgccccat ccgagatga cgtgaccaa 1200  
 gggcagcccc gagaaaccaca ggtgtacacc ctgccccat ccgagatga cgtgaccaa 1260  
 aaccaggtca gctgtacctg cctctctcta cagcaagctc accgtggaca agagcaggg 1320  
 tgggagagca atgggcagcc ggagaaacac tacaagacca cgctccctgt gctgactcc 1380  
 gacggtctct tcttctctta gatgcattag gctctgcaca accactacac gcagaagagc 1440  
 aacgtcttct catgtctcgt gatgcattag gctctgcaca accactacac gcagaagagc 1500  
 ctctccctgt ctcgggtaaa agcggatcct tcgaacctgc tcccatcctg gccattacc 1560  
 ttaattctag taatgtgaat ttttgtgata tgctgcctga cctactgctt tgcccaaga 1620  
 gaagaggaga gaaggaggaa tgagagattg agaagggaaa gtgtacgcc tgataaatc 1680  
 gat 1683

<210> 268  
 <211> 556  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 268  
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 1 5 10 15  
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
 20 25 30  
 Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala  
 35 40 45  
 Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln  
 50 55 60  
 Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn  
 65 70 75 80  
 Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 85 90 95  
 Asp Phe Ser Leu Asn Ile His Pro Val Gln Glu Asp Asp Ile Ala Met  
 100 105 110  
 Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly  
 115 120 125  
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly  
 130 135 140  
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly  
 145 150 155 160  
 Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly  
 165 170 175  
 Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Gly  
 180 185 190  
 Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp  
 195 200 205  
 Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Trp Lys Asp Asn Ser  
 210 215 220  
 Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr  
 225 230 235 240  
 Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr  
 245 250 255  
 Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
 260 265 270  
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro  
 275 280 285  
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys  
 290 295 300  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 305 310 315 320

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
325 330 335  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
340 345 350  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
355 360 365  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
370 375 380  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
385 390 400  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
405 410 415  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 425 430  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
480 485 490 495  
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu  
500 505 510  
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile  
515 520 525  
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg  
530 535 540 545  
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val  
550 555

<210> 269  
<211> 1665  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

<400> 269  
aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtcg ttcagtcata 60  
atgtccagag gagtgcacat ccagatgaca cagtctccat cctcagtcg tgcatctctg 120  
ggaggcaag tcacatcac agccaagaca agccaagaca ttaagaagta tatagttgg 180  
taccacaaca agcctggaaa aggtcccagg ctgtctatat attacacatc tacattacag 240  
caggcatcc catcaagggtt cagtggaaat gggctctggga gagattatct cctcagcatc 300  
agaaacctgg agcctgaaga tattgcaact tattattgtc aacagtatga taatcttcca 360  
ttgacgtttc gctcggggac aaagttggaa ataaaaacggg gtggcggtgg ctcgggcggt 420  
gggtgggtcgg gtggcgggcg atctgatgta cagcttcagg agtcaggacc tggcctcgtg 480  
aaactgttctc agtcttctctc tctcacctgc tctgtcactg gctactccat caccagtggt 540  
ttctacttga actggtatccg acagtttccg ggaacacaaa tggaaatggat gggtccacata 600  
agccacgacg gttaggaataa ctacaacca tctctcataa atcgaatctc catcactcgt 660  
gacacatctt agaaccagtt ttctctgaag ttgagttctg tgactactga ggacacagct 720  
acatatttct gtgcaagaca ctacggtagt acgggagcta tggactactg gggtcaacgga 780  
acctcagcta ccgtctctctc tgatctggag cccaaatctt ctgacaaaac tcacacatcc 840  
ccacgctccc cagcacctga actctctgggg ggatcgctcag tcttctctct cccccaaaa 900  
cccaaggaca cctcatgat ctcccggacc cctgaggtca catgcgttgtt ggtggacgtg 960  
agccacgaag accctgaggt caagttcac tggtagctgg acggcgtgga ggtgataat 1020  
gccaaagaca agccgcggga ggagcagtat aacagcacgt accgttgtgt cagctctc 1080  
accgtctctc accagagctg gctgaatggc aaggagtaaca agtccaaggt ctccaacaaa 1140  
gccctcccaag ccccatctga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200  
caggtgtata ccttcgcccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260  
tgctcgtgtca aaggcttctta tcccagcgac atcgccgtgg agtgggagag caatggcgag 1320  
ccgagaacca actacaagac cagcgtctcc gtgtctgact ccgacggctc cttcttctcc 1380  
tacagcaagc gctcagctgga caagagcagg tggcagcagg ggacgcttct ctatgctctc 1440  
gtgatgcatt aggtctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500  
aaagcgagtc cttcgaaact gctcccatcc tgggccatta ccttaattc gtctaaatgt 1560  
atttttggta tatgtgcctt gactcactgc ttgtcccaaa gatgcagaga gagaaggagg 1620  
aatgagagat tgagaaggga aagtgtacgc cctgtataaa tcgat 1665

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<210> 270  
<211> 550  
<212> PRT  
<213> Artificial sequence

<220>  
<223> fusion polypeptide

<400> 270  
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1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser  
20 25 30  
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala  
35 40 45  
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly  
50 55 60  
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu  
85 90 95  
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro  
145 150 155 160  
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr  
165 170 175  
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu  
180 185 190  
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro  
195 200 205  
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
210 215 220  
Phe Phe Leu Lys Leu Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr  
225 230 235 240  
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly  
245 250 255  
Gln Gly Thr Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser  
260 265 270  
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly  
275 280 285  
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
290 295 300  
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
305 310 315 320  
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
325 330 335  
His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr  
340 345 350  
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
355 360 365  
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
370 375 380  
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
385 390 395 400  
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
405 410 415  
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
420 425 430  
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
435 440 445  
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
450 455 460  
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
465 470 475 480  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
485 490 495  
Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr  
500 505 510  
Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys  
515 520 525  
Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg  
530 535 540  
Glu Ser Val Arg Pro Val  
545 550

<210> 271  
<211> 1653  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 271  
atgttgatata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60  
gacatagtgc tgactcagac tccagccact ctgtctctaa ttcttggaga aagagtcaca 120  
atgacctgta agacacagta gaattattggc acaattcttae actggtatca ccaaaaaacca 180  
aaggaggctc caaggogctc catcaagatg ctcttcagct ccattctctgg gatccccctc 240  
agattcagtg agattcagat ggaaacagat ttactctctc gcatacataa cctggagact 300  
gattgatactg gaatttattta ctgtcaacaa agtagaagct ggctgtcac gtcgggtctc 360  
ggcaccgaag cgagataaaa acggggtggc ggtggctcgg gcggaggtgg gtcgggtggc 420  
ggcggatctc aggtcaagct gcagcagctc ggttctgaa tagggaaacc tggggcctca 480  
gtgaaactgt cctgcaagac ttacagctac atattcacag atcattatat ttcttgggtg 540  
aaacagaagc ctggagaaga cctgcagctg atagaaaatg tttatgtgtg aaatgtgtgt 600  
acaagctaca atcaaaaatt ccagggcag gccacactga ctgtagataa aatctctagc 660  
acagcttaca tgggaactcag cagcctgaca tctgaggatt ctgccatcta ttactgtgca 720  
agaaggccgg tagcgacggg ccattgctat gactactggg gtcaggggat ccaagttacc 780  
gtctctctct atctggagcc caaatcttct gacaaaactc acacatcccc accgtcccca 840  
gcactggaac tcttgggggg atcgtcagtc ttctcttccc ccccaaaacc caaggacacc 900  
ctcatgtatc cccggacccc tgaggtcaca tgcgtgtgtg tggagctgag ccacgaagac 960  
cttgaggta agtcaacty gtacttggac ggcgtggagg tgcataatgc caagacaaag 1020  
ccgoggagg agcagtacaa cagacagtac ggtgtgtgtca ggcctctcac cgtcctgcac 1080  
caggaactggc tgaattggcaa ggaatcaca ggtcaaggct ccaacaaagc cctccagacc 1140  
ccattcgaga aaaccatctc caaagccaaa gggcagcccc gagaacacaa ggtgtacacc 1200  
ctgcccccac cccgggatga gctgaccaag aaccaggta cctgtgacct cctgtgtcaa 1260  
ggcttctatc ccagcgacat cgccgtggag tgggagagca gcgtgcagc ggagaaacac 1320  
tacaagacca gccttcccgt gctggaactc gacggctctt tcttctctca cagcaagctc 1380  
accgttggca agagcaggtg gcagcagggg aacgttctct catgtctcgt gatgcagtag 1440  
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa agcgaatctc 1500  
tcgaactctg tcccatcctg ggccattacc ttaattctcag taaatggaa ttttggata 1560  
tgctgacctg cctactgctt tgcccacaaga tgcagagaga gaaggaggaa tgagagattg 1620  
agaaggagaa gtgtacgccc tgtataaatc gat  
1653

<210> 272  
<211> 548  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 272  
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser  
1 5 10 15  
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser  
20 25 30  
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn  
35 40 45  
Ile Gly Thr Ile Leu His Thr Tyr His Gln Lys Pro Lys Glu Ala Pro  
50 55 60  
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser

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 65 70 75 80  
 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn  
 85 90 95  
 Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg  
 100 105 110  
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg  
 115 120 125  
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln  
 130 135 140  
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser  
 145 150 155 160  
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr  
 165 170 175  
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly  
 180 185 190  
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln  
 195 200 205  
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met  
 210 215 220  
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala  
 225 230 235 240  
 Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly  
 245 250 255  
 Ile Gln Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys  
 260 265 270  
 Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser  
 275 280 285  
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
 290 295 300  
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
 305 310 315 320  
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
 325 330 335  
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
 340 345 350  
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 355 360 365  
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 370 375 380  
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
 385 390 395 400  
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr  
 405 410 415  
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
 420 425 430  
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu  
 435 440 445  
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
 450 455 460  
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
 465 470 475 480  
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 485 490 495  
 Lys Ala Asp Pro Ser Asn Leu Leu Pro Trp Ala Ile Thr Leu Ile  
 500 505 510  
 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala  
 515 520 525  
 Pro Arg Cys Arg Glu Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser  
 530 535 540  
 Val Arg Pro Val  
 545

<210> 273  
 <211> 1521  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

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<223> fusion polynucleotide

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<400> 273
aagcttgccg ccattggatt tcaagtgcag attttcagct tcctgctaata cagtgcctca 60
gtcataattg ccagaggaca aattgttctc tccagttctc cagcaatcct gtctgcatct 120
ccaggggaga aggttcaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctgccccaac ccttgatttt atgccccatc caacctggct 240
cttgaggttc aggtctgaag tctgtccagg tattaactgc cctcttactc tctcaaatc 300
agcagagtgg aggtctgaag caagtctgag ctgaaagtgc gccagtgtagg ttttaacca 360
ccacgtttcg gtgctgggac ctctcaggct tatctcaagc agcgttggttc gggcggtgg 420
ggatctggag aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt tacactgtg 480
aggtctggag aatattgcact gggtaaaaca gacacctaga cagggtcctg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaagccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagg tgacatttga agactctgcg 720
gtctatttct gtgcaagagt gggttactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840
gacacattcc caccgtcccc agcacctgaa ctctgggggg gaccgtcagt ctctctcttc 900
ccccaaaac ccaaggacac cctcatgact tcctgggacc ctgagggtcac atgcgtgggt 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cgcgctggag 1020
gtgcataatt ccaagacaaa gccgcgggag gaggagtaca acagcagcta ccggtgtgct 1080
agcttctca ccgtctctgca ccctccagc ctgaaatgga aggagtacaa gtgcaaggtc 1140
tcgaacaaag aggtgtacac ccccatcgag aaaaacatct ccaagaccaa agggcagccc 1200
agcctgacct gacctgtcaa aggtctctac cccagcgata agctgaccaa gaaccaggtc 1260
aattggggcag cggaagaacaa ctacaagacc acgctctccg tcgctgtgga gtgggagagc 1320
ttcttctctc acagcaagct caccgtggac aagagcaggt ggcacaggg ctagcgcttc 1380
tcattgtcgc tgatgcattga ggctctgcac aaccactaca cgagaagag cctctcctcg 1440
ctccgggtta aatgatctg a

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<210> 274  
<211> 500  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

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<400> 274
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240

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<220>
<223> oligo to make IgG hinge CSS mutant using IgG hinge
      SSS as a template
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<400> 277
gtgttgatc aggagcccaa atcttgtagc aaaactcac      39

<210> 278
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to amplify constant regions for creating
      IgG hinge mutatnts

<400> 278
gtgtttcta gatcatttac ccggagacag ggagaggctc ttctgcgtgt ag      52

<210> 279
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligo that mutates VH11 L to S

<400> 279
ggaggtggga gctctcaggc ttatctacag cagtctgggg ctgagtcggt gaggcc      56

<210> 280
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo for amplifying IgG1 constant regions

<400> 280
gtctctagac tatcatttac ccggagacag      30

<210> 281
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for first PCR to insert IgA hinge into
      IgG1 CH2-CH3

<400> 281
ccatctccct caactccacc taccatctct cctcatgcg cacctgaact cctg      54

<210> 282
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for second PCR to insert IgA hinge into
      fused to IgG1 CH2

<400> 282
gtgttgatc agccagttcc ctcaactcca cctaccccat ctccccaact      50

<210> 283
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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<400> 283
aagcttgccg ccatggattt tcaagtcag attttcagct tcttgctaag cagtgtctca 60
gtcataattg ccagaggaca aattgttctc tccagctctc cagcaatcct gtctgcactct 120
cagggggaga aggtgacaat gacttgacag gccagctcaa gtgtaagtta catgcaactgg 180
taccagcaga agccaggatt cctcccaaaa cctctggatt atgccccatc caactctgggt 240
tctggagtc cctgctgctt cagtyggcagt gggctctggga cctcttaact tctcacaaatc 300
agcagagtgg aggtcgaaaga tgcctgcaact tattactgcc agcagtggaag ttttaaccca 360
cccaagcttcg gtgctgggag caagctggag ctgaagaatg gcggtggctc gggcggtgggt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgaactgggt 480
agggctgggg cctcagtgaa gatgtctctg aaggtctctg gctacacatt tccagttgat 540
aataatgcaat gggtaaaaga gacacctaga cagggtctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttacaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgcg 720
tctattttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctcg 780
ggcacaggga ccacgggtcac cgtctctgat cagccagttc cctcaactcc acctaccaca 840
tctccctcaa ctccacctac ccatctctcc tcatgcgcac ctgaaactct ggggggacgg 900
tcagtctctc tcttcccccc aaaaccacaag gacacctca tgatctcccg gacccctgag 960
gtcacatcgc tgggtgggga cgtgagccac gaagaccctg aggtcaagtt caactggtag 1020
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggagggaga ctacaaacgc 1080
acgtatccgtg tggtcagcgt cctcaccgtc ctgcaccaga actggctgaa tggcaaggag 1140
tacaagtcca aggtctccaa caaagccctc ccagcccca tcgagaaaac aatcttccaaa 1200
gccaaagggc agcccccaga accacagggtg tacacctctc ccccatcccg ggaatgagct 1260
accaagaacc aggtcagcct gactctgctg gtcaaaaggct tctatcccg cgacatgct 1320
gtggagtggg agagcaatgg gcagctggag aacactcagc agaccacgc tccctgctg 1380
gaactcgaag gctctctctt ctctacagc aagctcagc tggacaagag caggtggcag 1440
caggggaaag tcttctcatg ctccgtgatg catgaggtc tgcaacaaca ctacacgcag 1500
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<210> 284
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide
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<400> 284
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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
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http://www.uspto.gov/patent

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

245 250 255

Gly Thr Gly Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr  
260 265 270

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys  
275 280 285

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
290 295 300

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Arg Glu Val Thr Cys Val  
305 310 315 320

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
325 330 335

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
340 345 350

Gln Tyr Asn Ser Thr Tyr Arg Val Lys Val Leu Thr Val Leu His  
355 360 365

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
370 375 380

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
385 390 395 400

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
405 410 415

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 425 430

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475 480

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
485 490 495

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
500 505

<210> 285  
<211> 1584  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide  
  
<400> 285  
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gtcataattg ccagaggaca aattgtttct tcccgctctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagttta catgcactgg 180  
taccagcaga agccaggatc ctcccccaaa cctctggatt atgccccatc caactcggtc 240  
tctggagctc ctgctgcgtt cagtggcagt gggctgggga cctcttactc tctcacaaat 300  
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag tttaacca 360  
cccacgtctg gtgctgggac caagctggag ctgtacagc tatctacagc agctgggctc 420  
ggattctgag aggtggggag ctctcaggct gatctctgc aaggctctct gctacacatt taccagttac 480  
agccctgggg ctccagtga gacacctaga aagttcaagg agtctggggc tgaactgggt 540  
aatatgcact gggtaaagca ctacaatcag ctacatgcag ctacagcagc agtctgactt 600  
ccaggaaatg gtgatacttc ctacatgcag ctacagcagc agtctgactt agctatttat 660  
gacaaatctc ccagcacagc ctatgcagct ctacagcagc agtctgactt agctatttat 720  
gtctatttct ggcgaagagt ggtgtactat ctacagcagc agtctgactt agctatttat 780  
ggcacaggga ccacggttac cgtctcttct gatcacggag ttctcctaac tccacttacc 840  
ccatcttccc caactccacc taccactatc cctctatgct gccacccccg actgtcactg 900  
caccgacggg ccctcgaggga cctgtcttta ggttcaagg cgactctcac gtgcacactg 960  
accggccctga gagatgcctc aggtgtcacc ttcaactgga gccctcaag tgggaagagc 1020  
gctgttcaag gaccactgga cgtgacctc tgtggctgct acagcgtgtc cagtgtcctg 1080  
cgggctgtgt ccgagccatg gaaccatggg aaacacttca ctgtcactgc tgcctacccc 1140  
gagtcacaaga ccccgctaac gtccgagggag gtcgagggag gctgtgtgtc gctgtgtgtc 1200  
gtccacctgc ttggcttcaa cctgacttgg gtcgagggc gtcgagggc cagggccacc 1260  
tgctgtgtgt cgtgagaaga ctgacttgg gtcgagggc gtcgagggc gtcgagggc 1320  
gagctgtccc cgtgtgacag catactgcgc gtcgagggc gtcgagggc gtcgagggc 1380  
accactctct gcattgtggg ccacgagggc ctgcgctgg ccttcacaca gaagacatc 1440  
accttctctc gcattgtggg ccacgagggc ctgcgctgg ccttcacaca gaagacatc 1500

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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ggcacttgct actgataatc taga 1584

<210> 286  
<211> 520  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 286  
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1 5 10 15  
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser  
260 265 270  
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser  
275 280 285  
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu  
290 295 300  
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg  
305 310 315 320  
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser  
325 330 335  
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val  
340 345 350  
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr  
355 360 365  
Phe Thr Cys Thr Ala Ala Tyr Pro Gly Ser Lys Thr Pro Leu Thr Ala  
370 375 380  
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu  
385 390 395 400  
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr  
405 410 415  
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu  
420 425 430  
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser  
435 440 445  
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile

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 450 455 460  
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 465 470 475  
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile  
 485 490 495  
 Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met  
 500 505 510  
 Ala Glu Val Asp Gly Thr Cys Tyr  
 515 520

<210> 287  
 <211> 775  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 287  
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 tccctcatgc tgcaccccc gactgtcact gcacgcacgc gccctcgagg acctgtcttt 120  
 aggttcagaa gcgatccctca cgtgcacact gaccggcctg agagatgcct caggtgtcac 180  
 ctccacctgg acgcctctcaa gtgggaagag cctgtgtcaa ggaccacctt accgtgacct 240  
 ctgtgctctc tacagcgtgt ccagtgctct gccggcgtg gccgcagccat ggaaccatgg 300  
 gaagaccttc acctgcactg ctgcctacc cagatccaag accccgctaa ccgcaccct 360  
 ctcaaaatcc ggaacacat tccggcccga ggtccacctg ctgccgcgc cgtcggagga 420  
 ctggtgcctg aacgagctgg tgacgtctgac gtgcctggca cgtgcttca gccccaagga 480  
 tgtgtcgtgt cgtggtctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540  
 ggcatccggg caggagccca gccaggccac caccaccttc gctgtgacca gcatactgcg 600  
 cgtggcagcc gaggactgga agaaggggga cacttctccc tgcattgttg gccacgagc 660  
 cctgcgcgtg gccttcacac agaagaccat cgacgcctg gcgggtaaac ccaccatgt 720  
 caatgtgtct gttgtcatgg cggagtgga cggcacctgc tactgataat ctaga 775

<210> 288  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 288  
 Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro  
 1 5 10 15  
 Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg  
 20 25 30  
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys  
 35 40 45  
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr  
 50 55  
 Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu  
 65 70 75 80  
 Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro  
 85 90 95  
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser  
 100 105 110  
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg  
 115 120 125  
 Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn  
 130 135 140  
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp  
 145 150 155 160  
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys  
 165 170 175  
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr  
 180 185 190  
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys  
 195 200 205

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Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala  
210 215 220  
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val  
225 230 235 240  
Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr  
245 250

<210> 289

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR IgA hinge-CH2 CH3

<400> 289

gttgtttcta gattatcagt agcagggtgcc gtccacctcc gccatgacaa c

51

<210> 290

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 290

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acttcagga tcattcgttc ttccgaagat cctaagtagg acattgtgga gagaacatc 120  
cgaattattg ttctctgaa caacaggag aatatctctg atcccacctc accattgaga 180  
accagatttg tgtaccattt gtctgacctc agctgtaaaa aatgtgatcc tacagaagtg 240  
gagctggata atcagatagt tactgtctacc cagagcaata tctgtgatga agacagtgtc 300  
acagagacct gtcactatta tgacagaaac aagtgtcata cagctgtggt cccactcgta 360  
tatggtggtg agacacaaat ggtggaaaca gccttaacct cagatgcctg ctatcctgac 420  
taatctaga 429

<210> 291

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 291

Arg Ser Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys  
1 5 10 15  
Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn  
20 25 30  
Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn  
35 40 45  
Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val  
50 55 60  
Tyr His Leu Ser Asp Leu Ser Cys Lys Lys Cys Asp Pro Thr Glu Val  
65 70 75 80  
Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp  
85 90 95  
Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys  
100 105 110  
Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val  
115 120 125  
Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro  
130 135

<210> 292

<211> 36

<212> DNA

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<213> Artificial Sequence

<220>

<223> 5' oligo to PCR J chain

<400> 292

gtgttagat ctcaagaaga tgaaggatt gttctt 36

<210> 293

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR J chain

<400> 293

gtgttttcta gattagtcag gatagcaggc atctgg 36

<210> 294

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> 4 carboxy terminal amino acids deleted from IgA  
CH3

<400> 294

Gly Thr Cys Tyr  
1

<210> 295

<211> 763

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 295

tgatcagcca gtccctctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60

tcctctcatgc tgcacacccc gactgtcact gcaccgaccg gccctcgagg acctgtcttt 120

aggttcagaaa gcgacacctca cgtgcacact gaccggcctg agatagtcct caggtgtcac 180

cttcacctgg acgccctcaa gtgggaagag cgtgtttcaa ggaccacctg acctgtacct 240

ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccagacctt ggaaccatgg 300

gaagaccttc acttgcactg ctgcctaccc cgagtccaag acccgctaa ccgccacctt 360

ctcaaaatcc ggaacaacat tccggccgga gggtccacctg ctgccgcgcg cgtcggagga 420

gctggccctg aacgagctgg tgaacgtgac gtgcctggca cgtggcttca gccccaagga 480

tgtgtgggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540

ggcatcccgg caaggaccca gcaggggcac caccactctc gctgtgacca gcatactgcg 600

cgtggcagcg gaagactgga agaaggggga cactctcttc tgcatgggtg gccacgaggc 660

ctgcgcctgt gccctcacac agaagacat cgacccttg gcgggtaaac ccaccatgt 720

caatgtgtct gttgtcatgg cggaggtgga ctgataatct aga 763

<210> 296

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 296

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro

1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg

20 25 30

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50 55 60  
Pro Ser Ser Gly Lys Ser Val Gln Gly Pro Pro Asp Arg Asp Leu  
65 70 75 80  
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro  
85 90 95  
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser  
100 105 110  
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg  
115 120 125  
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn  
130 135 140  
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp  
145 150 155 160  
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys  
165 170 175  
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr  
180 185 190  
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys  
195 200 205  
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala  
210 215 220  
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val  
225 230 235 240  
Asn Val Ser Val Val Met Ala Glu Val Asp  
245 250

<210> 297

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo for construct with 4 amino acid deletion  
in IgA CH3

<400> 297

gtgtgttctca gattatcagt ccacctccgc catgacaaca gacac

45

<210> 298

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 298

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ccaggggaga aggtcacaat gactgtcagg gccagctcaa gtgtgaagta catgcaactgg 180  
taccagcaga agccaggatc ctcccacaaa ccttgattt atgcccacac caacctggct 240  
tcttgagctc ctgctcgctt cagtggcagt ggcctgggga cctcttactc tctcaaatc 300  
agcagagtgg agcctgaaga tgctgcact tattactgcc agcagtggag tttaacca 360  
cccacgtctg gtgctgggac caagctggag ctgaagaatg gcggtggctc ggcggtgg 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgg 480  
agcgtggggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt tacagttac 540  
aatatgcact gggtaagaca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttaacgg gcaaggccac actgactgta 660  
gacaaatcct ctacacagc ctacatgcag ctacagcagc tgacatctga agactctg 720  
gtctatttct ctgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctg 780  
ggcacaggga ccacggtcac ccacggtcac cctctatgct gccacccccc actgtcactg 840  
ccatctcctt caactccacc taccccatct cctctatgct gccacccccc actgtcactg 900  
caccagcggg cctcaggaga cctgtcttta gttcagaag cgatcctcac gtgcacactg 960  
accggcctga gagatgcctt aggtgtcacc ttcatctgga gcctctcaag tgggaagacg 1020  
gctgttcaag gaccacttga cgtgacctc ttgtgctgct acagcgtgtc cagtgtcctg 1080

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ccgggctgtg	ccgagccatg	gaaccatggg	aagaccttca	cttgactgct	tgccctaccc	1140
gagtcacaaga	ccccgcctaac	gcgccacctc	tcaaaatccg	gaaacacatt	ccggcccgag	1200
gtccacctgc	tgccgcgcgc	gtccgagggag	ctggccctga	acgagctggt	gacgctgacg	1260
tgcttgccac	gtggcttcag	cccccaaggat	gtgtggtgtc	gctggtctga	ggggtcacag	1320
gagctggccc	gcgagaagta	cctgacttgg	gcattccggc	aggagccag	ccagggcacc	1380
accaccttcg	ctgtgaccag	catactgcgc	gtggcagccg	aggactggaa	gaagggggag	1440
accttcttcc	gcattggtggg	ccacgagggc	ctgccgctgg	ccttcacaca	gaagaccatc	1500
gcggctgttg	gcggtaaac	caccatgtgc	aatgtgtctg	ttgtcatggc	ggaggtggag	1560
tgataatcta	ga					1572

<210> 299  
<211> 516  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 299

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
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			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
			35					40				45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
			50			55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65			70						75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85					90					95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	
		130				135						140			
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145			150						155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Thr	Phe	Thr	Ser	Tyr	
			165					170						175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
			180					185				190			
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195				200						205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
			210			215						220			
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225					230				235					240	
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
			245					250					255		
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Asp	Gln	Pro	Val	Pro	Ser
			260					265					270		
Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr	Ser	Ser	Pro	Ser
			275				280					285			
Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg	Pro	Ala	Leu	Glu	Asp	Leu
		290				295					300				
Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys	Thr	Leu	Thr	Gly	Leu	Arg
305					310				315					320	
Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr	Pro	Ser	Ser	Gly	Lys	Ser
			325						330					335	
Ala	Val	Gln	Gly	Pro	Pro	Asp	Arg	Asp	Leu	Cys	Gly	Cys	Tyr	Ser	Val
			340					345					350		
Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro	Trp	Asn	His	Gly	Lys	Thr
		355					360					365			
Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser	Lys	Thr	Pro	Leu	Thr	Ala
		370				375					380				
Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg	Pro	Glu	Val	His	Leu	Leu
385					390				395					400	

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr  
405 410 415  
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu  
420 425 430  
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser  
435 440 445  
Arg Gln Glu Pro Ser Gln Gly Thr Thr Phe Ala Val Thr Ser Ile  
450 455 460  
Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys  
465 470 475  
Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile  
485 490 495  
Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met  
500 505 510  
Ala Glu Val Asp  
515

<210> 300

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 14 amino acids deleted from IgAH-T4 (so that total  
of 18 amino acids deleted from wild type Iga CH3

<400> 300

Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp  
1 5 10

<210> 301

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo for engineering 14 amino acid from IgA-T4

<400> 301

gttgtttcta gattatcatt taccgcgcaa gcggtcgatg gtctt

45

<210> 302

<211> 709

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 302

tgatcagcca	gttccctcaa	ctccacctac	cccatctccc	tcaactccac	ctaccccatc	60
tccctcatgc	tgccaccccc	gactgtcact	gcaccgaccg	gccctcgagg	acctgtcttt	120
agggtcagaa	gcgatctcca	cgctgcacac	gaccggcctg	agagatgcct	cagggtgtcac	180
cttcacctgg	acgcctctcaa	gtgggaagag	cgctgttcaa	ggacacctg	acctgtacct	240
ctgtggctgc	tacagcgtgt	ccagtgtctc	gccgggctgt	gccgagccat	ggaaccatgg	300
gaagaccttc	acttgccatg	ctgcctacc	cgagtccaag	accccgctaa	ctgccacct	360
ctcaaaatcc	ggaacacat	tccggccrca	ggtccacctg	ctgccgcgcg	cgtcgaggga	420
gctggccctg	aacgagctgg	tgacgctgac	gtgcctggca	cgtggcttca	gccccaagga	480
tgctgtggtt	cgctggctgc	aggggtcaca	ggagctgccc	cgcgagaagt	acctgacttg	540
gcgcatccgg	caggagccca	gccaggccac	caccaccttc	gctgtgacca	cgatactcgg	600
cgtygcagcc	gaggactgga	agaaggggga	cactttctcc	tgcatggtgg	gccacaggac	660
ctcgcgctg	gcccttcacac	agaagaccat	cgaccgcttg	gcgggtgtaa		709

<210> 303

<211> 236

<212> PRT

<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polypeptide

<400> 303

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Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
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Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
20      25      30
Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
35      40      45
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
50      55      60
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
65      70      75      80
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
85      90      95
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100      105      110
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115      120      125
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130      135      140
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145      150      155      160
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
165      170      175
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
180      185      190
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
195      200      205
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210      215      220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
225      230      235

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<210> 304

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 304

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gtcataattg ccagaggaca aattgtcttc tccagttctc cagcaatcct gtctgcctct 120
ccaggggaga aggtcaccaat gacttgcagg gccagctcaa gtgtaagta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa cctctggatt atgccccatc caactctggt 240
cttggagctcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaaac 300
agcagagtgg agcctgaaga tgcctgccat tattactgcc agcagtggaag ttttaacc ca 360
cccacgtctg gtgctgggac caagtgggag ctgaaagatg gcggtggctc tggcggtggt 420
ggagtctggag gaggtgggag ctctcaggct tatctacacg agtctggggc tgagctgg tg 480
agggctgggg cctcagtgaa gatgtctctg aaggctctcg gctacacatt taccagttac 540
aatatgcact ggtgaagca gacacctaga caggcctggg aatggattgg agctattat 600
caggaaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatctc ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgct 720
gtctattttc gtcgaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggctac cgtctcttct gatcagccag ttccctcaac tccacctacc 840
ccatctctct caactccacc taccctatct cctcatgctt gccaccccg actgtctac 900
caccgaccgg cctctgagga cctgctctta ggttcagaag cgatctcaac gtgcacactg 960
accggctcga gagatgcctc ttaccttggg ttaccttggg cgccctcaag tgggaaga gc 1020
ctgtgttcaag gaccacttga cgtgtaccct tgtggctgct acagcgtgtc cagtgtctctg 1080
ccgggtctgt ccgagccatg gaacctggg aagaccttca cttgcactgc tgcctacc cc 1140
gagtcacaag ccccgctaac cgccaccctc tcaaaatccg gaaacacatt ccggcccg ag 1200
gtctcacctc tgcgcgcgc gtcggaggag ctggccctga acgagctggt gacgtgta gc 1260
tgctctggac gtggcttcag cctcaaggat gtgtggctgc gctggctgca ggggtcac ag 1320
gagctgcccc gcgagaagta cctgacttgg gcatcccgcc aggagccca ccaggga cc 1380

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
accacccttcg ctgtgaccag catactgcgc gtggcagccg aggactggaa gaagggggac 1440  
acccttctcct gcattgtggg ccacgagggc ctgcgcgtgg ccttcacaca gaagaccattc 1500  
gaccgcttgg cgggtaaa 1518

<210> 305

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 305

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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Arg Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260      265      270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275      280      285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290      295      300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305      310      315      320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325      330      335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340      345      350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355      360      365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370      375      380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385      390      395      400
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405      410      415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420      425      430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435      440      445
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Arg Gln Glu Pro Ser Gln Gly Thr Thr Phe Ala Val Thr Ser Ile  
 450 455 460  
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys  
 465 470 475 480  
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile  
 485 490 495  
 Asp Arg Leu Ala Gly Lys  
 500

<210> 306  
 <211> 924  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 306  
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 tccagtggaa atcaagtga cctcactatc caaggactga gggccatgga cacgggactc 120  
 tacatctgca aggtggagct catgtaccac ccgccatact acctgggcat agggcaacgga 180  
 acccagattt atgtaattga tccagaaccg tgcccagatt ctgatcaacc caaatcttgt 240  
 gacaaaactc acacaaagcc accgtgccca gcaactgaac tcctgggggg accgtcagtc 300  
 ttctctcttc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 360  
 tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 420  
 ggctgtgagg tgcataatgc caagacaag ccgctggagg agcagtaaca cagcacgtac 480  
 cgtgtgttca cgtctctcac cgtctctgac caggactggc tgaatggcaa ggagtacaag 540  
 tccaaggtct ccaacaagac ctctccagcc cccatcgaga aaacaatctc caaagccaaa 600  
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 660  
 aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 720  
 tggggagagca atggggacgc ggagaacaac tacaagacca cgctctccgt ctggactctc 780  
 gacggctctc ttctctctta cagcaagctc accgtggaca agagcaggtg gcacgagggg 840  
 aacgtctctc catgctccgt gatcgatgac gctctgcaca accactacac gcagaagagc 900  
 ctctccctgt ctccgggtaa atga 924

<210> 307  
 <211> 382  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 307  
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
 1 5 10 15  
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30  
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45  
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60  
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75  
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 80 85 90  
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110  
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125  
 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
 130 135 140  
 Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Cys Asp Lys Thr His Thr  
 145 150 155 160  
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 165 170 175  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
 180 185 190

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
 195 200 205  
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 210 215 220  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
 225 230 235  
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 245 250 255  
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 260 265 270  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 275 280 285  
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 290 295 300  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 305 310 315  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp  
 320 325 330  
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 335 340 345  
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 350 355 360  
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 370 375 380

<210> 308  
 <211> 453  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 308  
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 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggcc cagcagccga 120  
 ggcacgcga gctttgtgtg tgagtgatga tctccaggca aagccactga ggtccgggtg 180  
 acagctcttc ggcaggctga cagccagggt actgaagctc gtgcggcaac ctacatgatg 240  
 gggaatgagt tgaccttctt agatgattcc actgcacgg gacactcaat tgggaatcaa 300  
 gtgaacctca ctatcaagg actgagggcc atggacacgg gactctacat ctgcagggtg 360  
 gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420  
 attgatccag aaccgtgccc agattctgat caa 453

<210> 309  
 <211> 151  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 309  
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 1 5 10 15  
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 20 25 30  
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45  
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60  
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80  
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95  
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110  
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr  
 115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Gln
130 135 140
Pro Cys Pro Asp Ser Asp Gln
145 150

<210> 310
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for engineering 14 amino acids from
Iga-T4

<400> 310
gttgttgatc agccaggttcc ctcaactcca cctaccccat ctccctcaac t 51

<210> 311
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 311
atgggggttac tgctcacaca gaggacgtcg ctcaagtctgg tccttgcact cctgtttcca 60
agcatggcgga gcatg 75

<210> 312
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 312
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met
20

<210> 313
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 313
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gttgttgagt atgcattctcc aggcacaagcc actgaggtcc ggggacagt gcttcgggcag 120
gttgacagcc aggtgactga agtctgtgcg gcaacctaca tgacggggaa tgagttgacc 180
ttcttagatg attccattctg caggggcacc tccagtgga atcaagtgaa cttcactatc 240
caaggactga aggcactgga caggggactc tacattctga aggtggagct catgtacca 300
cgccatact acctgggcat aggcacgga acccagattt atgtaatga tccagaaccg 360
tgccagatt ct 372

<210> 314
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

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<400> 314

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1      5      10      15
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
20      25      30
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35      40      45
Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp
50      55      60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65      70      75      80
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
85      90      95
Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
100      105      110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
115      120

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<210> 315

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 315

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ggcatgcgca  gctttgtgtg  tgagtatgca  tctccaggca  aagcactcga  ggtccgggtg  180
acagtgcttc  ggcaggctga  cagccaggctg  actgaagctc  gtgcggcaac  ctacatgatg  240
gggaatgagt  tgaccttcct  agatgattcc  attcgcacgg  gcacctccag  tggaaatcaa  300
gtgaacctca  ctgaacctca  actgaggggc  atggacacgg  gactctacat  ctgcaaggty  360
gagctcatgt  acccaccgcc  atactacctg  ggcataggca  acggaaccca  gatttatgta  420
attgatccag  aaccgtgcc  agattctgat  caacccaaat  ctctgcacaa  aactcacaca  480
tccccaccgt  cccagaccc  tgacctctg  gggggatcgt  cagtcttctc  ctcccccca  540
aaaaccaagg  acaccctcat  gatctcccg  acccttgagg  tcacatgcgt  ggtggtggac  600
gtagccacag  aagaccctga  ggtcaagttc  aactcgtacg  tggacggcgt  ggaggtgcat  660
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ctcacccgtc  tgaccacga  ctggctgaat  ggcaaggagt  acaagtgcac  ggtctccaac  780
aaagccctcc  cagcccccac  cgagaaaaca  atctccaag  ccaagggca  gccccgagaa  840
ccacagggtg  acaccctgcc  ccatcccg  gatgagctga  ccaagaacca  ggtcagcctg  900
acctgctctg  tcaaaaggct  ctatccacg  gacatcgctg  tggagtggga  gagcaatggg  960
cagccggaga  acaactacaa  gaccacgct  cccgtgctgg  actccgacgg  ctctctcttc  1020
ctctacagca  agctcacctg  ggacaagagc  aggtggcagc  aggggaacgt  ctctcctcgt  1080
tcctgtatgc  atgaggctct  gcacaaccac  tacacgcaga  agagcctctc  cctgtctcgt  1140
ggtaaatga

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<210> 316

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 316

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Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1      5      10      15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20      25      30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35      40      45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50      55      60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65      70      75      80

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
85 90 95  
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
100 105 110  
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr  
115 120 125  
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
130 135 140  
Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Ser Asp Lys Thr His Thr  
145 150 155  
Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe  
165 170 175  
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
180 185 190  
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
195 200 205  
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
210 215 220  
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val ser Val  
225 230 235 240  
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
245 250 255  
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
260 265 270  
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
275 280 285  
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
290 295 300  
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
305 310 315 320  
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp  
325 330 335  
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
340 345 350  
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
355 360 365  
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375 380

<210> 317  
<211> 1221  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

<400> 317  
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agcatggcgga gcatggcaat gcacgtggcc cagcctgctg ttgtactggc cagcagcgga 120  
ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga gggtccgggtg 180  
acagtgcttc ggcaggctga cagccagggtg actgaagctc gtgcggcaac ctacatgatg 240  
gggaatgagt tgaccttctt actgaggttc acttgacacg gcacctccag tggaaatcaa 300  
gtgaacctca cctatccaag atactacctg ggcataccca gactctacat ctgcaagggtg 360  
gagctcatagt acccaccgct agattctgat cagccagttc cctcaactcc acctacccca 420  
attgatccag acccgtgccc ccatctctcc tcatgtctgc accccgact gtcaactgac 540  
ctctccctaa cctcacctac gctcttaggt tcagaagcga tctctacgtg cacactgacc 600  
cgaccggccc tcgaggacct gctcttaggt acctggagcg cctcaagtgg gaagagcgct 660  
ggcctgagag atgcctcagg tgctaccttc gggtgtccga cgtgtgccg gtctctgccg 720  
gttcaaggag cacttgaccg tgacctctgt gactctctga acattcttcg ctaccccgag 780  
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tccaagaccg cactaacgcg caccctctca ggcctgaacg agctggtgac gctgacgtgc 900  
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ttctcctga ttgtgggcca cgaggccctg ccgctggcct tcacacagaa gaccatcgac 1140  
cgcttgccgg gtaaacccac ccatgtcaat gtgtctgttg tcatggcaga ggttgacggg 1200

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
acctgctact gataatctag a 1221

<210> 318  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 318  
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20 25 30  
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
35 40 45  
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
50 55 60  
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
65 70 75 80  
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
85 90 95  
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
100 105 110  
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
115 120 125  
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
130 135 140  
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro  
145 150 155 160  
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg  
165 170 175  
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu  
180 185 190  
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val  
195 200 205  
Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro  
210 215 220  
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro  
225 230 235 240  
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala  
245 250 255  
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser  
260 265 270  
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Ser Glu  
275 280 285  
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly  
290 295 300  
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu  
305 310 315 320  
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser  
325 330 335  
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala  
340 345 350  
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu  
355 360 365  
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly  
370 375 380  
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly  
385 390 395 400  
Thr Cys Tyr

<210> 319  
<211> 1209  
<212> DNA  
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 319

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ggcatcgcca  gctttgtgtg  tgagtatgca  tctccaggca  aagccaactg  ggtccgggtg  180
acagtgcttc  ggcaggctga  cagtcagggt  actgaagctc  gtgcggcaac  ctacatgatg  240
gggaatgagt  tgaccttctc  agatgatgcc  actgcacggg  gcacctccag  tggaaatcaa  300
gtgaacctca  ctatccaagg  actgagggcc  atgcacggcg  acggaacca  gctcaatgta  360
gagctcatgt  acccaccgcc  atactacctg  ggcattagca  acggaacca  actaaccaca  420
attgatccag  aaccgtgccc  agattctgat  cagccagttc  cctcaactcc  actaaccaca  480
tcttccctcaa  ctccacctac  cccattctcc  tcctgctgcc  accccgact  gtcactgcac  540
cgaccggccc  tcgaggacct  gctcttagtg  tcagaagcga  tcctcacgtg  cacactgacc  600
ggcctgagag  atgcttcagg  tgtcaccttc  acctggagcg  cctcaagtgg  gaagagcgct  660
gttcaaggac  cacctgaccg  tgacctctgt  ggctgctaca  gcgtgtccag  tgtctctgcc  720
ggctgtgccg  agccatggaa  ccatgggaag  acctcactt  gcactgctgc  ctaccacggg  780
tccaagaccc  cgctaaccgc  caccctctca  aaatccggaa  acacttccg  gcccgaggtc  840
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ctgcgccgca  agaagtacct  gacttgggca  tcccgccagg  agcccagcca  gggcaccacc  1020
accttcctgc  tgaccagcat  actgcgcgtg  gcagccgagg  actggaagaa  gggggacacc  1080
ttctcttgca  tgggtggcca  gagggcctg  ccgctggcct  tcacacagaa  gaccactcaa  1140
cgcttggcgg  gtaaaaccac  ccatgtcaat  gttctgtgtg  tcattggcga  ggtggactga  1200
taattctaga

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<210> 320

<211> 399

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 320

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Leu  Leu  Phe  Pro  Ser  Met  Ala  Ser  Met  Ala  Met  His  Val  Ala  Gln  Pro
20          25          30          35
Ala  Val  Val  Leu  Ala  Ser  Ser  Arg  Gly  Ile  Ala  Ser  Phe  Val  Cys  Glu
35          40          45          50
Tyr  Ala  Ser  Pro  Gly  Lys  Ala  Thr  Glu  Val  Arg  Val  Thr  Val  Leu  Arg
50          55          60          65
Gln  Ala  Asp  Ser  Gln  Val  Thr  Glu  Val  Cys  Ala  Ala  Thr  Tyr  Met  Met
65          70          75          80
Gly  Asn  Glu  Leu  Thr  Phe  Leu  Asp  Asp  Ser  Ile  Cys  Thr  Gly  Thr  Ser
80          85          90          95
Ser  Gly  Asn  Gln  Val  Asn  Leu  Thr  Ile  Gln  Gly  Leu  Arg  Ala  Met  Asp
100         105         110         115
Thr  Gly  Leu  Tyr  Ile  Cys  Lys  Val  Glu  Leu  Met  Tyr  Pro  Pro  Pro  Tyr
115         120         125         130
Tyr  Leu  Gly  Ile  Gly  Asn  Gly  Thr  Gln  Ile  Tyr  Val  Ile  Asp  Pro  Glu
130         135         140         145
Pro  Cys  Pro  Asp  Ser  Asp  Gln  Pro  Val  Pro  Ser  Thr  Pro  Pro  Thr  Pro
145         150         155         160
Ser  Pro  Ser  Thr  Pro  Pro  Thr  Pro  Ser  Pro  Ser  Cys  Cys  His  Pro  Arg
160         165         170         175
Leu  Ser  Leu  His  Arg  Pro  Ala  Leu  Glu  Asp  Leu  Leu  Leu  Gly  Ser  Glu
175         180         185         190
Ala  Ile  Leu  Thr  Cys  Thr  Leu  Thr  Gly  Leu  Arg  Asp  Ala  Ser  Gly  Val
185         190         195         200
Thr  Phe  Thr  Trp  Thr  Pro  Ser  Ser  Gly  Lys  Ser  Ala  Val  Gln  Gly  Pro
200         205         210         215
Pro  Asp  Arg  Asp  Leu  Cys  Gly  Cys  Tyr  Ser  Val  Ser  Ser  Val  Leu  Pro
215         220         225         230
Gly  Cys  Ala  Glu  Pro  Trp  Asn  His  Gly  Lys  Thr  Phe  Thr  Cys  Thr  Ala
230         235         240         245
Ala  Tyr  Pro  Glu  Ser  Lys  Thr  Pro  Leu  Thr  Ala  Thr  Leu  Ser  Lys  Ser
245         250         255

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 260 265 270  
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 275 280 285  
 Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Glu  
 290 295 300  
 Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu  
 305 310 315  
 Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser  
 320 325 330  
 Gln Gly Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala  
 335 340 345  
 Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu  
 350 355 360  
 Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly  
 365 370 375  
 Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp  
 380 385 390 395

<210> 321  
 <211> 328  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 321  
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 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataagtcmaa gacaaagccg 180  
 cgggaggagc agtacaacag cagctaccgt gtggtcagcg tcctcaccgt cctgcaccag 240  
 gactggctga atggcaagga gtacaagtc aaggtctcca acaagaccct ccagccccc 300  
 atcgagaaaa ccactcctcaa agccaaag 328

<210> 322  
 <211> 109  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 322  
 Pro Glu Leu Leu Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro  
 1 5 10 15  
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 20 25 30  
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
 35 40 45  
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 50 55 60  
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 65 70 75 80  
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
 85 90 95  
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 100 105

<210> 323  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Amino acids surrounding the proline at 238

<400> 323

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
1 5 10

<210> 324  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Amino acid substitution of Serine for Proline at  
238

<400> 324  
Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser  
1 5 10

<210> 325  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' oligo to PCR IgE Fc

<400> 325  
gttggtgatc acgtctgctc cagggacttc acccc 35

<210> 326  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to PCR IgE Fc

<400> 326  
gttggttctta gattaacttt taccgggatt tacagacacc gctcgtcg 49

<210> 327  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligo to provide open reading frame at carboxy end  
of CH4 to read into transmembrane and cytoplasmic  
tail of another protein

<400> 327  
gttggttttcg aaggatccgc ttaccggga ttacagaca ccgctcgctg g 51

<210> 328  
<211> 996  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 328  
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cgacggcgcc gggcacttcc ccccgaccat ccagctccctg tgcctcgtct ctgggtacac 120  
cccaggpact atcaacatca cctggctgga ggaacgggcag gtcattggagc tggacttgctc 180  
cacgcctctt accacgcagg agggctgagct ggctctcaca caaagcgagc tcaccttcag 240  
ccagaagcac tggctgtctag accgcacctc cactctgcag gtcacctatc aaggtcacac 300  
ctttgagagc agcaccaaga agtggtgcaga ttccaacccg agaggggtga gcgcctacct 360  
aagccggccc agcccgttcg acctgttcat ccgcaagtcg ccacagatca cctgtctggt 420

WO 2005/037989

PCT/US2003/024918

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 gtccacctg ccggtgggca cccgagactg gatcgagggg gagacctacc agtgcagggt 600  
 gacccacccc cacttgccca gggccctcat gcggtccacg accaagacca gccggcccg 660  
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 caacgagtg cagctcccg acgcccggca cagcacgacg cagccccgca agaccaagg 840  
 ctccggcttc ttctgtctta gcgcttggg ggtgaccagg gccgaatggg agcagaaga 900  
 tgagttcatc tgcctgcag tccatgagc agcagcccc tcacagaccg tccagcgagc 960  
 ggtgtctgta aatcccggta aagcggatcc ttcgaa

<210> 329  
 <211> 331  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 329  
 Asp His Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu  
 1 5 10 15  
 Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu  
 20 25 30  
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Ser Thr Trp  
 35 40 45  
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr  
 50 55 60  
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser  
 65 70 75 80  
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr  
 85 90 95  
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn  
 100 105 110  
 Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro Phe Asp Leu  
 115 120 125  
 Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val Asp Leu Ala  
 130 135 140  
 Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala Ser Gly Lys  
 145 150 155 160  
 Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg Asn Gly Thr  
 165 170 175  
 Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp Trp Ile Glu  
 180 185 190  
 Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala  
 195 200 205  
 Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg Ala Ala Pro Glu  
 210 215 220  
 Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg  
 225 230 235 240  
 Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu Asp Ile Ser Val  
 245 250 255  
 Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala Arg His Ser Thr  
 260 265 270  
 Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Ser Arg  
 275 280 285  
 Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys  
 290 295 300  
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 305 310 315 320  
 Val Ser Val Asn Pro Gly Lys Ala Asp Pro Ser

<210> 330  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

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<400> 330
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acc 63

<210> 331
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 331
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<210> 332
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 332
gttggtgatc aggagcccaa atctcttgac aaaactcaca catctccacc gtccccagca 60
cctgaactcc tgggtggacc gtcagctcttc c 91

<210> 333
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 333
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ccaggggaga aggtcacaat gacttgacag gccagctcaa gtgtaagtta catgcaactgg 180
taccagcaga agccaggatc ctcccccaaa cctctggattt atgccccatc caactcgtgt 240
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ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatctc ccagcacagc ctacatgcag ctacagaccc tgacatctga agactctgctg 720
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ggcacaggga cacggtctac ctctctgtat ggtgtactat cactgactct cgtctgctgt 840
accgtgaaga tcttacagtc gtctctgcag ggcggcggtc acttccccct gccctgcctc 900
ctctctgtcc tctgtctggc gtacaccca cctcctacca cgcaggaggc tgagctggcc 960
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tgccaggctca ctatcaagg tcacaccttt gaggacagca ccaagaaggc tgcagatttc 1140
aaccgagagc ggtgatgcgc ctacctaagc cggccagacc cgttcgacct gttcatccgc 1200
aagtgcacca cgatcacctg tctggtggtg gactctgcac ccagcaaggc gacggtgaac 1260
ctgacctggt ccggggccag tgggaagcct gtgaaccact ccaccagaaa ggaggagaag 1320
cagcgcaatg gcacgttaac cgtcacgtcc accctgcggc tgggcacccg agactcgatc 1380
gagggggaga cctaccagtg cagggtgacc caccceacc tgcccagggc cctcatcgcc 1440
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gagtggccgg gggagcggga caagcgacc ctgcgctgcc tgatccagaa ctctatgcct 1560
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acgagcgagc ccgcacaag caaaggctcc tcttcagcgc cgtgcagctca tgaggcagcg 1680
accaggcgcc aatgggagca gaaagatgag ttcatctcgc gtgcagctca tgaggcagcg 1740
agccccctac agaccgtcca gcgagcgggt tctgtaaatc ccggtaaatg ataactctaga 1800

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<210> 334  
<211> 592  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> fusion polypeptide

<400> 334  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Asp His Val Cys Ser Arg Asp  
260 265 270  
Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly  
275 280 285  
Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr  
290 295 300  
Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met  
305 310 315 320  
Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala  
325 330 335  
Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp  
340 345 350  
Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp  
355 360 365  
Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr  
370 375 380  
Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr  
385 390 395 400  
Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn  
405 410 415  
Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg  
420 425 430  
Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu  
435 440 445  
Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg

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 450 455 460  
 Val Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys  
 465 470 475 480  
 Thr Ser Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro  
 485 490 495  
 Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln  
 500 505 510  
 Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val  
 515 520 525  
 Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys  
 530 535 540  
 Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu  
 545 550 555 560  
 Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala  
 565 570 575 580  
 Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys  
 580 585 590

<210> 335  
 <211> 339  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 335  
 acaggtgcagc tgaaggaggc aggcactggc ctggtgcaac cgacacagac cctgtccctc 60  
 acatgcactg tctctgggtt ctcattaacc agcgatgggt tacactggat tcgcacagcct 120  
 ccaggaaagg gttctggaatg gatgggaata atatattatg atggaggcac agattataat 180  
 tcagcaatta aatccagact gagcatcagc agggacacct ccaagagcca agttttctta 240  
 aaaatcaaca gtctgcaaac tgaatgacaca gccatgtatt actgtgccag aatccacttt 300  
 gattactggg gccaaaggat catggtcaca gtctcctct 339

<210> 336  
 <211> 321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 336  
 gacattgtgc tcaactcagtc tccaacaacc atagctgcat ctccagggga gaaggtcacc 60  
 atcacctgcc gtgccagctc cagtgttaagt tacatgtact ggtaccagca gaagtcaggc 120  
 gccctccccta aactctggat ttatgacaca tccaagtctg cttctggagt tccaatcgc 180  
 ttcagtggca gtgggtctgg gacctcttat tctctcgcaa tcaacacat ggagactgaa 240  
 gatgctgcca ctattactgt tcagcagctg agtagtact cgctcacgtt cgggtctggg 300  
 accaagctgg agatcaaacg g 321

<210> 337  
 <211> 785  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 337  
 aagcttatgg attttcaagt gcagattttc agcttctctg taatcagctg ttcagtcata 60  
 agttccagag gagtcgacat ttgtctcact cagtctccaa caacatagc tgcattccca 120  
 ggggagaagg tcaccatcac ctgccgtgac agctccagtg taagttaact gtactgtgac 180  
 cagcagaagt caggcgcttc cctaaactc tggatttatg acacatccaa gctggcttct 240  
 ggagttccaa atgccttcag tggcagtggt tctgggacct cttattctct cgcaatcac 300  
 accatggaga ctgaagatgc tggcacttat tactgtcagc agtgagtag tactctcgtc 360

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
acgttccgggt ctgggaccaa gctggagatc aaacgggggt gcggtggctt gggcggtgggt 420  
gggtcggggt gcggcggtatc tcaggtgcag ctgaaggagg caggacctgg cctggtgcaa 480  
cgacacaga cctgtccctt cacatgcact gtctcgggt tctcattaac cagcggtgggt 540  
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600  
gatggagga cagattataa ttcagcaatt aaatccagac tgagcatcag caggagacac 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaa ctgatgcac agccatgtat 720  
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780  
gatca 785

<210> 338  
<211> 1491  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 338  
aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtc ttcagtcata 60  
atgtccagag gactgcacat tgtgtcactt cagttctccaa caaccatagc tgcattccca 120  
ggggagaagg tcacatcac ctgcctggcc agctccagtg taagtattac gtactgtgtac 180  
cagcagaagt caggcgcttc ccttaaaact tggatttatg acacatccaa gctggctctct 240  
ggagttccaa atcgcttcag tggcagtggt tctgggacct ctattctctt cgcaatcaac 300  
accatggaga ctgaagatgc tgccacttat tactgtcagc agtgggatag tctactcgctc 360  
acggttcgggt ctgggaccaa gctggagatc aaacgggggt gcggtggctt gggcggtgggt 420  
gggtcggggt gcggcggtatc tcaggtgcag ctgaaggagg caggacctgg cctggtgcaa 480  
cgacacaga cctgtccctt cacatgcact gtctcgggt tctcattaac cagcgatgggt 540  
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600  
gatggagga cagattataa ttcagcaatt aaatccagac tgagcatcag caggagacac 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaa ctgatgcac agccatgtat 720  
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780  
gatccagagc caaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 840  
cttcctgggg gaccgtcagt ctctcctctt ccccaaaaac ccaaggacac cctcatgattc 900  
tcccgagccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga cctgagggtc 960  
aagttcaact ggtacgtgga cggctgagg gtgcataatg ccaagacaaa gcccgggagg 1020  
gagcagatca acagcaagta gtgtgtgttc cgtgtgtgtc cgtctctgca gccgtggtac 1080  
ctgaatggca agagatcaaa gtgcagagtc cgagaacac cccctccagc cccagactcgag 1140  
aaaaaactt ccaagaccaa agggcagccc agctgcactt agctgtacac aggtgtacac cctgcccaca 1200  
tcccgggagt agctgaccaa gaaccaggtg gctggagatc aaacgggggt gcggtggctt gggcggtgggt 420  
ccagcgaca tgcgcgtgga gtgggagagc aatggggcag cggagacaaa aggtctctat 1260  
acgcttccc tgctgtactt cgacggctcc ttctctctt acagcaagct caccgtggac 1380  
aagagcaggt ggacgagggt gaactgtctt tcatgtctcg tgatgcataa ggctctgcac 1440  
aaccactaca cgcagaagag cctctcctctg tctcgggta aatgatctag a 1491

<210> 339  
<211> 1645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 339  
aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtc ttcagtcata 60  
atgtccagag gactgcacat tgtgtcactt cagttctccaa caaccatagc tgcattccca 120  
ggggagaagg tcacatcac ctgcctggcc agctccagtg taagtattac gtactgtgtac 180  
cagcagaagt caggcgcttc ccttaaaact tggatttatg acacatccaa gctggctctct 240  
ggagttccaa atcgcttcag tggcagtggt tctgggacct ctattctctt cgcaatcaac 300  
accatggaga ctgaagatgc tgccacttat tactgtcagc agtgggatag tctactcgctc 360  
acggttcgggt ctgggaccaa gctggagatc aaacgggggt gcggtggctt gggcggtgggt 420  
gggtcggggt gcggcggtatc tcaggtgcag ctgaaggagg caggacctgg cctggtgcaa 480  
cgacacaga cctgtccctt cacatgcact gtctcgggt tctcattaac cagcgatgggt 540  
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600  
gatggagga cagattataa ttcagcaatt aaatccagac tgagcatcag caggagacac 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaa ctgatgcac agccatgtat 720  
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780  
gatctggagc ccaaatcttc tgacaaaact cacacaagcc caccgagccc agcatctgaa 840

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ctctctgggg gatcgctcagt cttcctcttc cccccaaaac ccaaggacac cctcatgattc 900  
tcccggaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccttgaggctc 960  
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gcccgggag 1020  
gagcagtcaca acagcacgtga cgtgtgggtc agcgtcctca cgtctctgca ccaggactgg 1080  
ctgaatggca aggaagtacaa gtgcaaggtc tccaacaaa cctctccagc ccccatcgag 1140  
aaaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccaca 1200  
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgtgcaa aggtctctat 1260  
cccagcgaca tcgctgtgga gtgggagagc aatgggcagc cggagaaaca ctacaagacc 1320  
acgctctccg tctggactc cgacggctcc ttctctctc acagcaagct caccgtggac 1380  
aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcg tgatgcatga ggctctgac 1440  
aaccaactca cgcagaagag cctctccctg tctccgggta aagcggatcc ttgcaacctg 1500  
ctcccatcct gggccattac cttaatctca gtaaatggaa tttttgtgat atgctgcctg 1560  
acctactgct ttgcccaca atgcagagag agaaggagga atgagagatt gagaaggaaa 1620  
agtgtacgcc ctgtataaat cgata

<210> 340  
<211> 1645  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

<400> 340  
aagcttatgg attttcaagt gcagattttc agcttctctc taatcagtcg ttcagtcata 60  
agttccagag agtcgacat tgggtcactc agtctcccaa caaccatagc tgactggtac 120  
ggggagaaag tcacatcac ctgcctgccc agctccagtg taagttacat gtaactggtac 180  
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa cctggtctct 240  
ggagttccaa atcgcttcag tggcagtggt tctgggacct cttattctct cgcaactaac 300  
accatctgaga ctgaagatgc tgccacttat tactgtcagc agtggaatga tactccgctc 360  
acgttccgggt ctgggaccaa gctggagatc aaacgggggt gcggtggctc gggcggtgtg 420  
gggtcgggtg cggcggtgat cagggtgcag ctgaaggagg caggacctgg cctggtgcaa 480  
cgacacagaa cctctgcctc cacatgcact gtctctgggt tctcattaac cagcgatggt 540  
gtacacttga ttcgacagag ggtctggaat ggatgggaat aatatattat 600  
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaaccc 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgcac agccattgat 720  
tactgtgcca gaatccactt tgaattactg ggccaaggag tcatgtgcac agtctcctct 780  
gatctggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgcc agcacctgaa 840  
ctctcggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgattc 900  
tcccggaccc ctgagtcac atgcgtgggt gtggacgtga gccacgaaga ccttgaggctc 960  
aagttcaact gtaagtgga cggcgtggag gtgcataatg ccaagacaaa gcccgggag 1020  
gagcagtcaca acagcacgtga cgtgtgggtc agcgtcctca cgtctctgca ccaggactgg 1080  
ctgaatggca aggaagtacaa gtgcaaggtc tccaacaaa cctctccagc ccccatcgag 1140  
aaaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccaca 1200  
tcccgggatg agctgaccaa gaaccaggtc agcctgacct agctgtgcaa aggtctctat 1260  
cccagcgaca tcgctgtgga gtgggagagc aatgggcagc cggagaaaca ctacaagacc 1320  
acgctctccg tctggactc cgacggctcc ttctctctc acagcaagct acccggtgac 1380  
aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcg tgatgcatga ggctctgac 1440  
aaccaactca cgcagaagag cctctccctg tctccgggta aagcggatcc ttgcaacctg 1500  
ctcccatcct gggccattac cttaatctca gtaaatggaa tttttgtgat atgctgcctg 1560  
acctactgct ttgcccaca atgcagagag agaaggagga atgagagatt gagaaggaaa 1620  
agtgtacgcc ctgtataaat cgata

<210> 341  
<211> 113  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> fusion polypeptide

<400> 341  
Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr Gln  
1 5 10 15  
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asp  
20 25 30  
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile Lys  
50 55 60  
Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe Leu  
65 70 75 80  
Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala  
85 90 95  
Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser  
100 105 110  
Ser

<210> 342  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 342  
Asp Ile Val Leu Thr Gln Ser Pro Thr Thr Ile Ala Ala Ser Pro Gly  
1 5 10 15  
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met  
20 25 30  
Tyr Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp Ile Tyr  
35 40 45  
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Asn Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Ser Tyr Ser Leu Ala Ile Asn Thr Met Glu Thr Glu  
65 70 75 80  
Asp Ala Ala Thr Tyr Cys Gln Gln Trp Ser Ser Thr Pro Leu Thr  
85 90 95  
Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

<210> 343  
<211> 258  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 343  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr  
20 25 30  
Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
35 40 45  
Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala  
50 55 60  
Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
65 70 75 80  
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
85 90 95  
Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
115 120 125  
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
145 150 155 160  
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
165 170 175  
Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 180 185 190  
 Met Gly Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser

<210> 344  
 <211> 492  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 344  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr  
 20 25 30  
 Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
 35 40 45  
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Lys Ser Gly Ala  
 50 55 60  
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
 65 70 75 80  
 Pro Asn Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
 85 90 95  
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
 115 120 125  
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 130 135 140  
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
 145 150 155 160  
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
 165 170 175  
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 180 185 190  
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 260 265 270  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 275 280 285  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 290 295 300  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 305 310 315 320  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 325 330 335  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 340 345 350  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 355 360 365  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

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49076.000004pct2 10.207.655 seq List Text 07.24.03.txt  
 370 375 380  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 385 390 395 400  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 405 415  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 420 425 430  
 Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser  
 435 440 445  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 450 455 460  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 465 470 475 480  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 485 490

<210> 345

<211> 543

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 345

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr  
 20 25 30  
 Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
 35 40 45  
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala  
 50 55 60  
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
 65 70 75 80  
 Pro Asn Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
 85 90 95  
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
 115 120 125  
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 130 135 140  
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
 145 150 155 160  
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
 165 170 175  
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 180 185 190  
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 260 265 270  
 Pro Cys Pro Ala Pro Glu Leu Leu Glu Gly Pro Ser Val Phe Leu Phe  
 275 280 285  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 290 295 300  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 305 310 315 320  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 325 330 335  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

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Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
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Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
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115      120      125
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Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
80
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
95
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
125
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
140
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
155
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
170
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
185
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
200
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
215
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
230
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Ser Asn Ser Glu
245
Glu Ala Lys Lys Glu Glu Ala Lys Lys Glu Glu Ala Lys Lys Ser Asn
260
Ser Val Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr
275
Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser
290
Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu
305
Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly Ile Pro Ser Arg Phe
320
Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val
335
Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln His His Ser Phe
350
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly
365
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Ile Gln
380
Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Arg
400
Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Thr Gly Met Gln
415
Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile Gly Trp Ile
430
Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu Gln Gly Arg
445
Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile
460
Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys Val Arg Ser
475
Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp Gly Gln Gly
490
Thr Leu Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr
505
His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Gly Gly Ser Ser
520
545
560

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565 570 575  
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
580 585 590  
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
595 600 605  
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
610 615  
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
625 630 635  
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
645 650 655  
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
660 665 670  
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
675 680 685  
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
690 695 700  
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
705 710 715 720  
Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
725 730 735  
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
740 745 750 755  
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
755 760 765

<210> 351  
<211> 1521  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

<400> 351  
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gtcataattg ccagaggaca aattgttctc tccagctctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtacaat gacttgcagg gccagctcaa gtgtgaagta catgcactgg 180  
taccagcaga agccaggatc ctccccaaa ccctggattt atgcccata caactggctt 240  
tctggagtcc ctgctcgctt cagtggcagt gggctgggga cctcttactc tccacaatc 300  
agcagagtgg aggtcgaaga tgctgccact tattactgcc agcagtggaag ttttaacca 360  
ccccagtctg gtctggggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420  
ggatctggag gaagtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480  
aggtctgggg cctcagtgaa gatgtcctgc aaggctctcg gctacacatt taccagttac 540  
aatatgcact gggtaaaaga gacacataga caggggctgg aatgatttgg agctatttat 600  
ccaggaaatg gtgatacttc ctacatcgag ctacatcgag ctacagagcc tgacatctga agactctcgy 720  
gacaaaatct ctgcaagagt gtgcaggtac agcacctgaa agtcaactctt agtactcttt 780  
gtctattctt ctcaggtcac cactgtcccc gatcaggagc ccaactcttc ttgacaaact 840  
cacacatccc caccgtcccc caagagacac cctcctgggg gatcgctcagt ctctctcttc 900  
ccccaaaac ccagagacac cctcctgggg ggaagctcac atgctgggtg 960  
gtggagctga gccacgaaga cctcctggag ggtacgtgga cggcgtggag 1020  
gtgcataatg ccaagacaaa cctcctggag ggtacgtgga cggcgtggag 1080  
agcgtctcca ccgtcctgca ccaggactgg ctgaattgga agggagacaa gtgcaaggtc 1140  
tgcacagaga cccctccagc cccatcgag aaaaacactc ccaagccaa agggcagccc 1200  
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260  
aggtcgacct cctgggtcaa aggtctctat cccagcgaga tcgcctgata gtggagagac 1320  
aatgggacag cggagaacaa ctacaagacc acgctctccc tgctggactc cgacggctcc 1380  
ttcttctctc acagacaagt caccgtggac aagagcaggt ggacagcagg gaactgtctc 1440  
tcattctctg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctcctg 1500  
ttctcgggta aatgatctag a

<210> 352  
<211> 500  
<212> PRT  
<213> Artificial Sequence

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 <220>  
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 <400> 352  
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 ser Pro Gly Lys  
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<210> 353  
<211> 423  
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<220>  
<223> fusion polynucleotide

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tgacacagct ctgtgtttctc attaatcacc tatgctgtac actgggttctg ccagctctcca 180  
ggaaagggtc tggagtggtt gggagtgata tggagtggtg gaatcacaga ctataatgca 240  
ctgtttcatat ccagactgag catcaccaag gacgattcca agagccaagt tttctttaaa 300  
atgaacagtc tgcaacctaa tgacacagcc atttattact gtgccagaaa tgggggtgat 360  
aactaccctt attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 420  
tca 423

<210> 354  
<211> 366  
<212> DNA  
<213> qArtificial Sequence

<220>  
<223> fusion polynucleotide

<400> 354  
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acctgcacag tctctgtgtt ctcatatact acctatgctg tacactgggt tcgcagctct 120  
ccaggaagag gctctggagt gctgggagtg atatggagtg gtggaatcac agactataat 180  
cagcttttca tatccagact gacatcaccc aaggacgatt ccaagagcca agttttcttt 240  
aaaatgaaca gttctgaacc taatgacaca gctctattat actgtgccag aaatgggggt 300  
gataactacc ctattacta tgctatggac tactggggtc aaggaaacct agtcaccgtc 360  
tcctca 366

<210> 355  
<211> 399  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 355  
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gatatttgta tgacgcaggc tgcatctctc aatccagtc cctctggaa ctcagctctc 120  
atctctctga ggtctagtta gactctctta catagtaatg gcatacctta tttgtattgg 180  
tatctgcaga agccaggcca gtctctctcag ctctcgattt atcagatgtc caaccttgcc 240  
tcaggagctc cagagaggtt cagttagcagt gggtcaggaa ctgatttcac atgagaatc 300  
acagagtggt aggtcaggga tgtgggtgtt tattactgtg ctcaaaatct agaacttcg 360  
ctcagcttct gtcgtgggac caagctggag ctgaaacgg

<210> 356  
<211> 825  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 356  
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ggatccactg catagattgt gatgacgcag gctgcattct ccaatccagt cactctctga 120  
acatcagctt cactctctctg caggtctagt aagagctctc tacatagtaa tggcatcact 180  
tatttgtatt ggtatctgca gaagccaggc cagctctctc agctctctat tatcagagt 240  
ctcaaccctt cctcaggagt ccagacaggg ttcatgagca gtgggtcagg atcagatttc 300  
acactgagaa tcagcagagt ggaggtcagg gatgtgggt ttattactgt tgcctaaaat 360  
ctagaacttc cgtccagctt cgggtgctgg accaagctgg agctgaaacg ggggtgcggt 420